

OM protein - protein search, using sw model

Run on: July 6, 2004, 14:19:41 ; Search time 64 Seconds
(without alignments)
3964.495 Million cell updates/sec

Title: US-10-624-932-2
Perfect score: 4791
Sequence: 1 MAVRPGLWLPALLGIVLAAWL.....AVAGLGQPDAGLFTVSEAE 898

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	4791	100.0	898	5	AAU85403	Aau85403 Human pro
2	4781	99.8	898	5	AAU97899	Aau97899 Human net
3	4698.5	98.1	899	5	AAU79939	Aau79939 Human UNC
4	4638	96.8	898	2	AAW78898	Aaw78898 Rat UNC-5
5	4638	96.8	898	5	AAU10543	Aau10543 Rat netri
6	4638	96.8	898	5	AAU97900	Aau97900 Rat netri
7	4526.5	94.5	943	4	AAM79128	Aam79128 Human pro
8	4413	92.1	842	5	AAU74818	Aau74818 Human REP
9	2815	58.8	556	2	AAW78899	Aaw78899 Human UNC

10	2755	57.5	931	4	AAB50691	Aab50691	Human	UNC
11	2755	57.5	931	7	ADE63098	Ade63098	Human	Pro
12	2755	57.5	982	4	ABG11551	Abg11551	Novel	hum
13	2578.5	53.8	945	7	ADE63096	Ade63096	Rat	Prote
14	2571.5	53.7	943	2	AAW78900	Aaw78900	Rat	UNC-5
15	2563.5	53.5	933	5	AAO18734	Aao18734	Human	NOV
16	2563.5	53.5	933	5	AAO18735	Aao18735	Human	NOV
17	2558.5	53.4	945	4	AAU12244	Aau12244	Human	PRO
18	2558.5	53.4	945	6	ABO17688	Abo17688	Novel	hum
19	2558.5	53.4	945	6	ABU80942	Abu80942	Human	PRO
20	2558.5	53.4	945	6	ABU66642	Abu66642	Human	PRO
21	2558.5	53.4	945	6	ABU59723	Abu59723	Novel	sec
22	2558.5	53.4	945	6	ABO24913	Abo24913	Human	sec
23	2558.5	53.4	945	6	ABU66918	Abu66918	Human	sec
24	2558.5	53.4	945	6	ADA45665	Ada45665	Novel	hum
25	2558.5	53.4	945	6	ADA76096	Ada76096	Human	PRO
26	2558.5	53.4	945	6	ADA18746	Ada18746	Human	PRO
27	2558.5	53.4	945	6	ADA61369	Ada61369	Homo sapi	
28	2558.5	53.4	945	6	ADB19154	Adb19154	Novel	hum
29	2558.5	53.4	945	6	ADB27695	Adb27695	Human	PRO
30	2558.5	53.4	945	6	ADA86174	Ada86174	Novel	hum
31	2558.5	53.4	945	6	ADB15738	Adb15738	Human	PRO
32	2558.5	53.4	945	6	ADA47524	Ada47524	Human	PRO
33	2558.5	53.4	945	6	ADA67319	Ada67319	Human	PRO
34	2558.5	53.4	945	6	ADB30326	Adb30326	Human	PRO
35	2558.5	53.4	945	6	ADA85622	Ada85622	Novel	hum
36	2558.5	53.4	945	6	ADA96834	Ada96834	Human	PRO
37	2558.5	53.4	945	6	ADA79138	Ada79138	Human	PRO
38	2558.5	53.4	945	6	ADA87277	Ada87277	Novel	hum
39	2558.5	53.4	945	6	ADB16479	Adb16479	Human	PRO
40	2558.5	53.4	945	6	ADA91571	Ada91571	Novel	hum
41	2558.5	53.4	945	6	ADB14634	Adb14634	Human	PRO
42	2558.5	53.4	945	6	ADB18595	Adb18595	Novel	hum
43	2558.5	53.4	945	6	ADA93810	Ada93810	Human	PRO
44	2558.5	53.4	945	6	ADB19706	Adb19706	Novel	hum
45	2558.5	53.4	945	6	ADB13018	Adb13018	Human	PRO

ALIGNMENTS

RESULT 1

AAU85403

ID AAU85403 standard; protein; 898 AA.

XX

AC AAU85403;

XX

DT 21-MAY-2002 (first entry)

XX

DE Human protein NOV1.

XX

KW Human; NOVX; cardiomyopathy; atherosclerosis; diabetes;

KW cell signal processing disorder; metabolic disorder; obesity; infection;

KW anorexia; cancer-associated cachexia; cancer; neurodegenerative disorder;

KW Alzheimer's disease; Parkinson's disease; immune disorder;

KW haematopoietic disorders; dyslipidaemia; pain; asthma; hypertension;

KW osteoporosis; Crohn's disease; multiple sclerosis; angina pectoris;

KW myocardial infarction; ulcer; allergy; benign prostatic hypertrophy;
 KW psychosis; neurological disorder; anxiety; schizophrenia;
 KW manic depression; dementia; dyskinesia; Huntington's disease;
 KW Gilles de la Tourette's syndrome; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200210216-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 30-JUL-2001; 2001WO-US024225.
 XX
 PR 28-JUL-2000; 2000US-0221409P.
 PR 04-AUG-2000; 2000US-0222840P.
 PR 04-AUG-2000; 2000US-0223752P.
 PR 04-AUG-2000; 2000US-0223762P.
 PR 04-AUG-2000; 2000US-0223769P.
 PR 04-AUG-2000; 2000US-0223770P.
 PR 14-AUG-2000; 2000US-0225146P.
 PR 15-AUG-2000; 2000US-0225392P.
 PR 15-AUG-2000; 2000US-0225470P.
 PR 16-AUG-2000; 2000US-0225697P.
 PR 01-FEB-2001; 2001US-0263662P.
 PR 05-APR-2001; 2001US-0281645P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Padigar M, Mezes P, Mishra V, Burgess C, Casman S, Grosse WM;
 PI Alsobrook JP, Lepley DM, Gerlach VL, Macdougall JR, Smithson G;
 XX
 DR WPI; 2002-180074/23.
 DR N-PSDB; ABK37922.
 XX
 PT New isolated cytoplasmic, nuclear, membrane bound, or secreted
 PT polypeptide, useful for treating cardiomyopathy, atherosclerosis,
 PT infections, cancer, neurodegenerative, metabolic, hematopoietic and
 PT immune disorders.
 XX
 PS Claim 1; Page 11; 213pp; English.
 XX
 CC The invention relates to an isolated cytoplasmic, nuclear, membrane
 CC bound, or secreted polypeptide (NOVX, x= 1-14) their variants or mature
 CC form. Also included are the nucleic acids encoding the NOVX proteins, a
 CC vector comprising the nucleic acid, a cell comprising the vector, an anti
 CC -NOVX antibody and modulators of NOVX. NOVX, the nucleic acid and the
 CC antibody are useful for treating or preventing a NOVX-associated
 CC disorder, where the disorder is selected from cardiomyopathy,
 CC atherosclerosis, diabetes, a disorder related to cell signal processing
 CC and metabolic pathway modulation, metabolic disorders, obesity,
 CC infectious disease, anorexia, cancer-associated cachexia, cancer,
 CC neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,
 CC immune disorders, haematopoietic disorders, and the various
 CC dyslipidaemias, metabolic disturbances associated with obesity, the
 CC metabolic syndrome X and wasting disorders associated with chronic
 CC diseases, bacterial, fungal, protozoal and viral infections, pain,
 CC bulimia, asthma, hypertension, urinary retention, osteoporosis, Crohn's

CC disease, multiple sclerosis, Albright Hereditary Osteodystrophy, angina
CC pectoris, myocardial infarction, ulcer, allergy, benign prostatic
CC hypertrophy, and psychotic and neurological disorders, including anxiety,
CC schizophrenia, manic depression, delirium, dementia, and dyskinesias,
CC such as Huntington's disease and Gilles de la Tourette's syndrome. The
CC nucleic acid is useful in gene therapy. The present sequence represents a
CC NOVX protein

XX

SQ Sequence 898 AA;

Query Match 100.0%; Score 4791; DB 5; Length 898;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 898; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP	60
Db	1	MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP	60
Qy	61	VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQVEKVFGL	120
Db	61	VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQVEKVFGL	120
Qy	121	EYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPGEGIPPAE	180
Db	121	EYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPGEGIPPAE	180
Qy	181	VEWLRNEDLVDPISLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAIVY	240
Db	181	VEWLRNEDLVDPISLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAIVY	240
Qy	241	VNGGWSTWTEWSVCSASCGRGWQKRSRSCNTPAPLNGGAFCEGQNVQKTACATLCPVDGS	300
Db	241	VNGGWSTWTEWSVCSASCGRGWQKRSRSCNTPAPLNGGAFCEGQNVQKTACATLCPVDGS	300
Qy	301	WSPWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDRNCTSDLCVHSASGPEDVA	360
Db	301	WSPWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDRNCTSDLCVHSASGPEDVA	360
Qy	361	LYVGLIAVAVCLVLLLLVLILVYCRKKEGLSDVDADSSILTSFGFQPVSIKPSKADNPHLL	420
Db	361	LYVGLIAVAVCLVLLLLVLILVYCRKKEGLSDVDADSSILTSFGFQPVSIKPSKADNPHLL	420
Qy	421	TIQPDLSSTTTTYQGSLCPRQDGPSPKFQLTNGHLLSPLGGGRHTLHHSSPTSEAEFVS	480
Db	421	TIQPDLSSTTTTYQGSLCPRQDGPSPKFQLTNGHLLSPLGGGRHTLHHSSPTSEAEFVS	480
Qy	481	RLSTQNYFRSLPRGTSNMTYGTFFNLGGRLMIPNTGISLLIPPDAIPRGKIYEIYTLHK	540
Db	481	RLSTQNYFRSLPRGTSNMTYGTFFNLGGRLMIPNTGISLLIPPDAIPRGKIYEIYTLHK	540
Qy	541	PEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDWSLRLKKQSCEGSW	600
Db	541	PEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDWSLRLKKQSCEGSW	600
Qy	601	EDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVAARKLKLFFAPVACT	660
Db	601	EDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVAARKLKLFFAPVACT	660

Qy 661 SLEYNIRVYCLHDT HDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRSLIHDVPSSLW 720
 |||||
 Db 661 SLEYNIRVYCLHDT HDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRSLIHDVPSSLW 720
 |||||
 Qy 721 KSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINF 780
 |||||
 Db 721 KSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINF 780
 |||||
 Qy 781 NITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISLDPPCRRGADWRTLAQKL 840
 |||||
 Db 781 NITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISLDPPCRRGADWRTLAQKL 840
 |||||
 Qy 841 HLDSHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAEC 898
 |||||
 Db 841 HLDSHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAEC 898
 |||||

RESULT 2

AAU97899

ID AAU97899 standard; protein; 898 AA.

XX

AC AAU97899;

XX

DT 27-AUG-2002 (first entry)

XX

DE Human netrin binding membrane receptor UNC5H-1 protein.

XX

KW Netrin binding membrane receptor; receptor; UNC5H-1; human; nootropic;

KW neuroprotective; cytostatic; antiparkinsonian; cerebroprotective; cancer;

KW central nervous system; CNS; stroke; Parkinson's disease;

KW multiple sclerosis; Alzheimer's disease.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 152. .223

FT /note= "Immunoglobulin domain "

FT Domain 247. .294

FT /note= "Thrombospondine type 1 domain "

FT Domain 302. .348

FT /note= "Thrombospondine type 1 domain"

FT Region 361. .382

FT /note= "Transmembrane region"

FT Domain 495. .598

FT /note= "ZU5 domain"

FT Domain 817. .897

FT /note= "Death domain"

XX

PN WO200233080-A2.

XX

PD 25-APR-2002.

XX

PF 15-OCT-2001; 2001WO-EP011891.

XX

PR 16-OCT-2000; 2000US-0240061P.

XX

PA (FARB) BAYER AG.
 XX
 PI Koehler RH;
 XX
 DR WPI; 2002-463314/49.
 DR N-PSDB; ABK52891.
 XX
 PT Novel human netrin binding membrane receptor polypeptide and
 PT polynucleotides for identifying modulating agents useful in treating
 PT diseases e.g. Parkinson's disease, multiple sclerosis, stroke,
 PT Alzheimer's disease.
 XX
 PS Claim 1; Fig 2; 94pp; English.
 XX
 CC This invention relates to the DNA and protein sequences of a novel
 CC purified human netrin binding membrane receptor, UNC5H-1. The DNA
 CC sequence of the invention is useful as a probe for detecting a nucleic
 CC acid encoding the UNC5H-1 protein in a biological sample. The sequences
 CC of the invention are useful to screen for agents which decrease the
 CC activity of the UNC5H-1 protein. The sequences are also useful for
 CC screening agents which regulate (modulate) the activity of the protein of
 CC the invention. A pharmaceutical composition containing the protein of the
 CC invention or a reagent that modulates the activity of the UNC5H-1 protein
 CC may be useful for treating a UNC5H-1 dysfunction related disease such as
 CC cancer or a central nervous system (CNS) disorders (e.g, Parkinson's
 CC disease, multiple sclerosis, stroke and Alzheimer's disease). Fusion
 CC proteins comprising the UNC5H-1 protein are useful for generating
 CC antibodies and for in various assay systems, and the protein can be used
 CC as a bait protein in a two-hybrid assay or three-hybrid assay. The method
 CC of the invention is useful for detecting a coding sequence for the UNC5H-
 CC 1 protein. The present sequence represents the human netrin binding
 CC membrane receptor UNC5H-1 protein of the invention
 XX
 SQ Sequence 898 AA;

Query Match 99.8%; Score 4781; DB 5; Length 898;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 896; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP 60
          |||
Db      1 MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP 60

Qy     61 VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQVEKVFGLE 120
          |||
Db     61 VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQVEKVFGLE 120

Qy    121 EYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPGIPPAE 180
          |||
Db    121 EYWCQCVAWSSSGTTKSQKAYIRIAYLRKNFEQEPLAKEVSLEQGIVLPCRPPGIPPAE 180

Qy    181 VEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAIVIVY 240
          |||
Db    181 VEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAIVIVY 240

Qy    241 VNGGWSTWTEWSVCSASCGRGWQKRSRSCCTNPAPLNGGAFCEGQNVQKTACATLCPVDGS 300
          |||

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Db	241	VNGGWSTWTEWSVCSASCGRGWQKRSRSCCTNPAPLNGGAFCEGQNVQKTACATLCPVDGS	300
Qy	301	WSPWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDTNRCTSDLCVHSASGPEDVA	360
		:	
Db	301	WSPWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDTNRCTSDLCVHTASGPEDVA	360
Qy	361	LYVGLIAVAVCLVLLLLVLILVYCRKKEGLSDVDADSSILTSGFQPVSIKPSKADNPHLL	420
Db	361	LYVGLIAVAVCLVLLLLVLILVYCRKKEGLSDVDADSSILTSGFQPVSIKPSKADNPHLL	420
Qy	421	TIQPDLSSTTTTYQGSCLPRQDGSPKQLTNGHLLSPLGGGRHTLHHSSPTSEAEFVS	480
Db	421	TIQPDLSSTTTTYQGSCLPRQDGSPKQLTNGHLLSPLGGGRHTLHHSSPTSEAEFVS	480
Qy	481	RLSTQNYFRSLPRGTSNMTYGTFFNLGGRLMIPNTGISLLIPDAIPRGKIYEIYLT LHK	540
Db	481	RLSTQNYFRSLPRGTSNMTYGTFFNLGGRLMIPNTGISLLIPDAIPRGKIYEIYLT LHK	540
Qy	541	PEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDSSWLRLLKKQSCEGSW	600
Db	541	PEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDSSWLRLLKKQSCEGSW	600
Qy	601	EDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVAARKLKL L FAPVACT	660
Db	601	EDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVAARKLKL L FAPVACT	660
Qy	661	SLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSSLW	720
Db	661	SLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSSLW	720
Qy	721	KSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINF	780
Db	721	KSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINF	780
Qy	781	NITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISSLDPPCRRGADWRTLAQKL	840
Db	781	NITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISSLDPPCRRGADWRTLAQKL	840
Qy	841	HLDSHLSFFASKPSPTAMILNLWEARHFNGNLSQLAAAVAGLGQPDAGLFTVSEAE	898
Db	841	HLDSHLSFFASKPSPTAMILNLWEARHFNGNLSQLAAAVAGLGQPDAGLFTVSEAE	898

RESULT 3

AAU79939

ID AAU79939 standard; protein; 899 AA.

XX

AC AAU79939;

XX

DT 15-JUL-2002 (first entry)

XX

DE Human UNC5-like protein NOV1.

XX

KW Human; NOVX polypeptide; cardiomyopathy; atherosclerosis; cancer;
 KW cell signal processing; metabolic pathway modulation; cancerous tissue;
 KW antibody; diabetes; transgenic animal; UNC5-like protein; NOV1;
 KW chromosome 13.

XX
 OS Homo sapiens.
 XX
 PN WO200229038-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 04-OCT-2001; 2001WO-US031377.
 XX
 PR 04-OCT-2000; 2000US-0237862P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Herrmann JL, Rastelli L, Shimkets RA;
 XX
 DR WPI; 2002-340104/37.
 DR N-PSDB; ABK49422.
 XX
 PT Novel isolated NOVX polypeptide, and encoded polynucleotide, useful for
 PT treating cardiomyopathy, artherosclerosis, and cancer.
 XX
 PS Claim 1; Page 9; 180pp; English.
 XX
 CC The present invention relates to a new NOVX polypeptide having a 900
 CC (NOV1), 4349 (NOV2), 940 (NOV3), 798 (NOV4), 865 (NOV5), or 331 (NOV6)
 CC residue amino acid sequence, as given in the specification. The novel
 CC polypeptide, and its encoding polynucleotide, are used to treat
 CC cardiomyopathy, atherosclerosis, cancer or a disease related to cell
 CC signal processing and metabolic pathway modulation, in a human. Detecting
 CC the polypeptide or polynucleotide is useful for identifying cancerous
 CC tissue. The antibody can be used to treat diabetes or cancer. The host
 CC cells can be used to produce non-human transgenic animals useful in drug
 CC screening. The present amino acid sequence is that of the human UNC5-like
 CC protein NOV1 of the invention. This sequence is encoded by the human UNC5
 CC -like NOV1 gene located on chromosome 13
 XX
 SQ Sequence 899 AA;

Query Match 98.1%; Score 4698.5; DB 5; Length 899;
 Best Local Similarity 98.7%; Pred. No. 0;
 Matches 888; Conservative 2; Mismatches 7; Indels 3; Gaps 3;

Qy	1	MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP	60
Db	1	MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP	60
Qy	61	VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSQQVEKVFGL	120
Db	61	VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGSEPTMEVRINVSQQVEKVFGL	120
Qy	121	EYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPEGIPPAE	180
Db	121	EYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPEGIPPAE	180
Qy	181	VEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAIVY	240
Db	181	VEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAIVY	240

Qy	241	VNGGWSTWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNV-QKTACATLCPVDG	299
Db	241	VNGGWSTWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVHDRVSSLLVSVDG	300
Qy	300	SWSPWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDRNCTSDLCVHSASGPEDV	359
Db	301	SWSPWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDRNCTSDLCVHSASGPEDV	360
Qy	360	ALYVGLIAVAVCLVLLLLVLILVYCRKKEGLDSDVADSSILTSFGQPVSIKPSKADNPHL	419
Db	361	ALYVGLIAVAVCLVLLLLVLILVYCRKKEGLDSDVADSSILTSFGQPVSIKPSKADNPHL	420
Qy	420	LTIQPDLSTTTTTYQGS LCP RQDGPSPKFQLTNGHLLSPLGGGRHTLHHSSPTSEAEFV	479
Db	421	LTIQPDLSTTTTTYQGS LCP RQDGPSPKFQLTNGHLLSPLGGGRHTLHHSSPTSEAEFV	479
Qy	480	SRLSTQNYFRSLPRGTSNMTYGTNF LGGRLMIPNTGISLLIPDAIPRGKIYEIYTLH	539
Db	480	SRLSTQNYFRSLPRGTSNMTYGTNF LGGRLMIPNTGISLLIPDAIPRGKIYEIYTLH	539
Qy	540	KPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDWSLRLKKQSCEGS	599
Db	540	KPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDWSLRLKKQSCEGS	599
Qy	600	WE-DVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVA AAKRLKLLLFAPVA	658
Db	600	WEQDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVA AAKRLKLLLFAPVA	659
Qy	659	CTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSS	718
Db	660	CTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSS	719
Qy	719	LWKS KLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSI	778
Db	720	LWKS KLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSI	779
Qy	779	NFNITKDTRFAELLAL ESEAGVPALVGPSAFKIPFLIRQKIISSLDPPCRRGADWRTL AQ	838
Db	780	NFNITKDTRFAELLAL ESEAGVPALVGPSAFKIPFLIRQKIISSLDPPCRRGADWRTL AQ	839
Qy	839	KLHLD SHLSFFASKPSPTAM I LNLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAE C	898
Db	840	KLHLD SHLSFFASKPSPTAM I LNLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAE C	899

RESULT 4

AAW78898

ID AAW78898 standard; protein; 898 AA.

XX

AC AAW78898;

XX

DT 25-MAR-2003 (revised)

DT 21-DEC-1998 (first entry)

XX

DE Rat UNC-5 homologue UNC5H-1.

XX

KW UNC-5; UNC5H-1; rat; netrin receptor; cell migration; axon guidance;
 KW diagnosis; therapy.
 XX
 OS Rattus sp.
 XX
 FH Key Location/Qualifiers
 FT Peptide 580. .594
 FT /note= "peptide used to raise rabbit polyclonal antisera"
 XX
 PN WO9837085-A1.
 XX
 PD 27-AUG-1998.
 XX
 PF 19-FEB-1998; 98WO-US003143.
 XX
 PR 19-FEB-1997; 97US-00808982.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Tessier-Lavigne M, Leonardo ED, Hinck L, Masu M, Keinomasu K;
 XX
 DR WPI; 1998-495364/42.
 DR N-PSDB; AAV52940.
 XX
 PT Netrin-binding, vertebrate proteins - useful for diagnosis, therapy and
 PT the biopharmaceutical industry.
 XX
 PS Claim 1; Page 19-22; 32pp; English.
 XX
 CC UNC5H-1 and UNC5H-2 (see AAW78900) are rat homologues of Caenorhabditis
 CC elegans UNC-5 protein. Their amino acid sequences were deduced from
 CC isolated unc5h cDNA clones (see AAV52940 and AAV52942) isolated from an
 CC E18 brain cDNA library. The predicted proteins show similarity with UNC-
 CC 5, possess 2 predicted Ig-like domains and 2 predicted thrombospondin
 CC type-1 repeats, a predicted membrane spanning region, and a large
 CC intracellular domain. They are predicted to be involved in cell migration
 CC and axon guidance, and are characterised as receptor proteins for
 CC netrins. Human UNC5H-1 (see AAW78899) and UNC5H-2 (see AAW78901) proteins
 CC are also claimed. Vertebrate UNC-5 proteins may be produced recombinantly
 CC from transfected host cells. The invention also provides unc-5
 CC hybridisation probes and primers, vertebrate UNC-5-specific binding
 CC agents such as specific antibodies, and methods of making and using the
 CC subject compositions in diagnosis (e.g. genetic hybridisation screens for
 CC vertebrate unc-5 transcripts), therapy (e.g. gene therapy to modulate
 CC vertebrate unc-5 gene expression) and in the biopharmaceutical industry
 CC (e.g. as immunogens, reagents for modulating cell guidance, reagents for
 CC screening chemical libraries for lead pharmacological agents, etc.).
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 898 AA;

Query Match 96.8%; Score 4638; DB 2; Length 898;
 Best Local Similarity 96.0%; Pred. No. 0;
 Matches 862; Conservative 17; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP 60
 |||

Db 1 MAVRPGLWPVLLGIVLAAWLRGSGAQQSATVANFPVPGANPDLLPHFLVEPEDVYIVKNKP 60

Qy 61 VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQVEKVFGL 120
 |||

Db 61 VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDSSSGLPTMEVRINVSRRQVEKVFGL 120
 |||

Qy 121 EYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPGEGIPPAE 180
 |||

Db 121 EYWCQCVAWSSSGTTKSQKAYIRIAYLRKNFEQEPLAKEVSLEQGIVLPCRPPGEGIPPAE 180
 |||

Qy 181 VEWLNRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAIVIVY 240
 |||

Db 181 VEWLNRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSTSAIVIVY 240
 |||

Qy 241 VNGGWSTWTEWSVCSASCGRGWQKRSRSCNTPAPLNGGAFCEGQNVQKTACATLCPVDGS 300
 |||

Db 241 VNGGWSTWTEWSVCSASCGRGWQKRSRSCNTPAPLNGGAFCEGQNVQKTACATLCPVDGS 300
 |||

Qy 301 WSPWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDTNRCTSDLCVHSASGPEDVA 360
 |||

Db 301 WSSWSKWSACGLDCTHWSRECSDPAPRNGGEECRGADLDTRNCTSDLCCLHTASCPEDVA 360
 |||

Qy 361 LYVGLIAVAVCLVLLLLLVLIIVYCRKKEGLDSDVADSSILTSQFQPVSIKPSKADNPHLL 420
 |||

Db 361 LYIGLVAVAVCLFLLLLLALGLIYCRKKEGLDSDVADSSILTSQFQPVSIKPSKADNPHLL 420
 |||

Qy 421 TIQPDLSSTTTTYQGSLSRQDGPSPKFQLTNGHLLSPLGGGRHTLHSSPTSEAEFVS 480
 |||

Db 421 TIQPDLSSTTTTYQGSLSRQDGPSPKFQLSNGHLLSPLGGRHTLHSSPTSEAEFVS 480
 |||

Qy 481 RLSTQNYFRSLPRGTSNMTYGTFFNLGGRLMIPNTGISLLIPPDAIPRGKIYEIYTLHK 540
 |||

Db 481 RLSTQNYFRSLPRGTSNMAYGTFFNLGGRLMIPNTGISLLIPPDAIPRGKIYEIYTLHK 540
 |||

Qy 541 PEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDSSWSRLKKQSCEGSW 600
 |||

Db 541 PEDVRLPLAGCQTLLSPVVSCGPPGVLLTRPVILAMDHCGEPSPDSSWSRLKKQSCEGSW 600
 |||

Qy 601 EDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVAARKLKLFFAPVACT 660
 |||

Db 601 EDVLHLGEESPSHLYYCQLEAGACYVFTEQLGRFALVGEALSVAATKRLRLLFFAPVACT 660
 |||

Qy 661 SLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHVPSSLW 720
 |||

Db 661 SLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHVPSSLW 720
 |||

Qy 721 KSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINF 780
 |||

Db 721 KSKLLVSYQEIPFYHIWNGTQQYLHCTFTLERINASTSDLACKVWVWQVEGDGQSFNINF 780
 |||

Qy 781 NITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISSLDPPCRGADWRTLAQKL 840
 |||

Db 781 NITKDTRFAELLALESEGGVPALVGPSAFKIPFLIRQKIIASLDPPCSRGAADWRTLAQKL 840
 |||

Qy 841 HLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAE 898
 |||

Db 841 HLDShLSFFASKPSPTAMILNLWEARHFPNGNLGQLAAAVAGLGQPDAGLFTVSEAE 898
 |||

RESULT 5

AAU10543

ID AAU10543 standard; protein; 898 AA.

XX

AC AAU10543;

XX

DT 14-FEB-2002 (first entry)

XX

DE Rat netrin receptor UNC5H1 (YSG7) polypeptide.

XX

KW YSG; YSG7; schizophrenia; chronic animal model; LCGU; netrin receptor;
KW local cerebral glucose utilisation; phosphodiesterase 1-alpha; UNC5H1;
KW calcium-independent alpha-latrotoxin receptor; CIRL; trkE; synapsin 1A;
KW epithelial discoidin domain receptor 1; synapsin 1B; neuroleptic;
KW tumour necrosis factor alpha; TNF-alpha; rat.

XX

OS Rattus sp.

XX

PN WO200175440-A2.

XX

PD 11-OCT-2001.

XX

PF 02-APR-2001; 2001WO-GB001486.

XX

PR 31-MAR-2000; 2000GB-00007880.

PR 26-MAY-2000; 2000GB-00012768.

XX

PA (WELF-) WELFIDE CORP.

XX

PI Cochran S, Paterson G, Ohashi Y, Morris B, Pratt J;

XX

DR WPI; 2002-010813/01.

DR N-PSDB; AAS16843.

XX

PT Novel chronic animal model of schizophrenia, useful for identifying anti-
PT psychotic drugs and genes that are associated with schizophrenia.

XX

PS Disclosure; Fig 8b; 79pp; English.

XX

CC The invention relates to YSG polynucleotide fragments for use in
CC diagnosing and/or developing treatments for schizophrenia using chronic
CC animal models. The polynucleotides and their encoded polypeptides are
CC used for identification of compounds which modulate the expression of YSG
CC molecules, leading to the manufacture of schizophrenia medicaments. The
CC sequences can also be used for testing candidate compounds for any effect
CC on the polypeptides. Anti-schizophrenic effects of a compound can be
CC determined by measuring local cerebral glucose utilisation (LCGU) or
CC comparing its expression level with that of a control group. The
CC sequences are useful in the identification of genes associated with
CC schizophrenic states and in the development of an antibody. The sequences
CC of the invention include phosphodiesterase 1-alpha, calcium-independent
CC alpha-latrotoxin receptors (CIRL)-1,2&3, epithelial discoidin domain
CC receptor 1 (trkE), netrin receptor (UNC5H1), synapsins 1A and AB and
CC tumour necrosis factor (TNF) alpha. This sequence represents rat netrin
CC receptor UNC5H1 (YSG7) polypeptide

XX

SQ Sequence 898 AA;

Query Match 96.8%; Score 4638; DB 5; Length 898;

Best Local Similarity 96.0%; Pred. No. 0;

Matches 862; Conservative 17; Mismatches 19; Indels 0; Gaps 0;

```
Qy      1 MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP 60
        |||
Db      1 MAVRPGLWPVLLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP 60

Qy     61 VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQVEKVFGL 120
        |||
Db     61 VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDSSSGLPTMEVRINVSRRQVEKVFGL 120

Qy    121 EYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPEGIPPAE 180
        |||
Db    121 EYWCQCVAWSSSGTTKSQKAYIRIAYLRKNFEQEPLAKEVSLEQGIVLPCRPEGIPPAE 180

Qy    181 VEWLRNEDLVDP SLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAAVIVY 240
        |||
Db    181 VEWLRNEDLVDP SLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSTSAAVIVY 240

Qy    241 VNGGWSTWTEWSVCSASCGRGWQKRSRSC TNPAPLNGGAFCEGQNVQKTACATLCPVDGS 300
        |||
Db    241 VNGGWSTWTEWSVCSASCGRGWQKRSRSC TNPAPLNGGAFCEGQNVQKTACATLCPVDGS 300

Qy    301 WSPWSKWSACGLDCTHWSRECS DPAPRNGGEECQGTDLDRNCTSDLCVHSASGPEDVA 360
        || |||
Db    301 WSSWSKWSACGLDCTHWSRECS DPAPRNGGEECRGADLDRNCTSDLC LHTASCPEDVA 360

Qy    361 LYVGLIAVAVCLVLLLLVLILVYCRKKEGLDSDVADSSILTS GFQPVSIKPSKADNP HLL 420
        ||: ||| ||| | |: |||
Db    361 LYIGLVAVAVCLFLLLLALGLIYCRKKEGLDSDVADSSILTS GFQPVSIKPSKADNP HLL 420

Qy    421 TIQPD LSTTTTTYQGS LCP RQDGPSPKFQ LTN GHLLSPLGGGRHTLHHSSPTSEAE EFVS 480
        |||
Db    421 TIQPD LSTTTTTYQGS LCSRQDGPSPKFQ LSN GHLLSPLGSGRHTLHHSSPTSEAE D FVS 480

Qy    481 RLSTQNYFRSLPRGTSNM TYGTFN FLGGRLMIPNTGISLLIPPD AIPRGKIYEIY LTLHK 540
        |||
Db    481 RLSTQNYFRSLPRGTSNMAYGTFN FLGGRLMIPNTGISLLIPPD AIPRGKIYEIY LTLHK 540

Qy    541 PEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPD SWSLRLKKQSCEGSW 600
        |||
Db    541 PEDVRLPLAGCQTLLSPV VSCGPPGVLLTRPVILAMDHCGEPSPD SWSLRLKKQSCEGSW 600

Qy    601 EDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVA AAKRLKLLLFAPVACT 660
        |||
Db    601 EDVLHLGEEAPSHLYYCQLEAGACYVFTEQLGRFALVGEALSVA ATKRLRLLLFAPVACT 660

Qy    661 SLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSSLW 720
        |||
Db    661 SLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSSLW 720

Qy    721 KSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSD LACKLWVWQVEGDGQSFSINF 780
        |||
```

Db 721 KSKLLVSYQEIPFYHIWNGTQQYLHCTFTLERINASTSDLACKVWVWQVEGDGQSFNINF 780

QY 781 NITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISLDPPCRRGADWRTLAQKL 840
 |||||:|||||

Db 781 NITKDTRFAELLALESEGGVPALVGPSAFKIPFLIRQKIIASLDPPCSRGADWRTLAQKL 840

QY 841 HLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAE 898
 |||||

Db 841 HLDShLSFFASKPSPTAMILNLWEARHFPNGNLGQLAAAVAGLGQPDAGLFTVSEAE 898

RESULT 6

AAU97900

ID AAU97900 standard; protein; 898 AA.

XX

AC AAU97900;

XX

DT 27-AUG-2002 (first entry)

XX

DE Rat netrin binding membrane receptor UNC5H-1 protein.

XX

KW Netrin binding membrane receptor; receptor; UNC5H-1; Rat; nootropic;
 KW neuroprotective; cytostatic; antiparkinsonian; cerebroprotective; cancer;
 KW central nervous system; CNS; stroke; Parkinson's disease;
 KW multiple sclerosis; Alzheimer's disease.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT Domain 152. .223

FT /note= "Immunoglobulin domain "

FT Domain 247. .294

FT /note= "Thrombospondine type 1 domain "

FT Domain 302. .348

FT /note= "Thrombospondine type 1 domain"

FT Region 361. .382

FT /note= "Transmembrane region"

FT Domain 495. .598

FT /note= "ZU5 domain"

FT Domain 817. .897

FT /note= "Death domain"

XX

PN WO200233080-A2.

XX

PD 25-APR-2002.

XX

PF 15-OCT-2001; 2001WO-EP011891.

XX

PR 16-OCT-2000; 2000US-0240061P.

XX

PA (FARB) BAYER AG.

XX

PI Koehler RH;

XX

DR WPI; 2002-463314/49.

XX

PT Novel human netrin binding membrane receptor polypeptide and

Db	361	LYIGLVAVAVCLFLLLLLALGLIYCRKKEGLDSDVADSSILTSQFQVSIKPSKADNPHELL	420
Qy	421	TIQPDLSSTTTTYQGSLCPRQDGPSPKFQLTNGHLLSPLGGGRHTLHHSSPTSEAEFVS	480
		:	
Db	421	TIQPDLSSTTTTYQGSLCSRQDGPSPKFQLSNHLLSPLGSGRHTLHHSSPTSEAEFVS	480
Qy	481	RLSTQNYFRSLPRGTSNMTYGTFFNLGGRLMIPNTGISLLIPDAIPRGKIYEIYLT LHK	540
		:	
Db	481	RLSTQNYFRSLPRGTSNMTYGTFFNLGGRLMIPNTGISLLIPDAIPRGKIYEIYLT LHK	540
Qy	541	PEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDWSLRLKKQSCEGSW	600
		:	
Db	541	PEDVRLPLAGCQTLLSPVVSCGPPGVLLTRPVILAMDHCGEPSPDWSLRLKKQSCEGSW	600
Qy	601	EDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVAARKRLKLLFAPVACT	660
		:	
Db	601	EDVLHLGEEAPSHLYYCQLEAGACYVFTEQLGRFALVGEALSVAATKRLRLLLFAPVACT	660
Qy	661	SLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDPSSLW	720
		:	
Db	661	SLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDPSSLW	720
Qy	721	KSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINF	780
		: : :	
Db	721	KSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERINASTSDLACKLWVWQVEGDGQSFNINF	780
Qy	781	NITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISSLDPPCRRGADWRTLAQKL	840
		:	
Db	781	NITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIIASLDPPCSRGAADWRTLAQKL	840
Qy	841	HLDSHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAEAC	898
		:	
Db	841	HLDSHLSFFASKPSPTAMILNLWEARHFPNGNLGQLAAAVAGLGQPDAGLFTVSEAEAC	898

RESULT 7

AAM79128

ID AAM79128 standard; protein; 943 AA.

XX

AC AAM79128;

XX

DT 06-NOV-2001 (first entry)

XX

DE Human protein SEQ ID NO 1790.

XX

KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.

XX

OS Homo sapiens.

XX

PN WO200157190-A2.

XX

PD 09-AUG-2001.

XX

PF 05-FEB-2001; 2001WO-US004098.

```
XX      03-FEB-2000; 2000US-00496914.
PR      27-APR-2000; 2000US-00560875.
PR      20-JUN-2000; 2000US-00598075.
PR      19-JUL-2000; 2000US-00620325.
PR      01-SEP-2000; 2000US-00654936.
PR      15-SEP-2000; 2000US-00663561.
PR      20-OCT-2000; 2000US-00693325.
PR      30-NOV-2000; 2000US-00728422.
XX
PA      (HYSE-) HYSEQ INC.
XX
PI      Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI      Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI      Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR      WPI; 2001-476283/51.
DR      N-PSDB; AAK52261.
XX
PT      Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT      in diagnosis and gene therapy.
XX
PS      Claim 20; Page 4148-4150; 6221pp; English.
XX
CC      The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC      encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC      cytokine, cell proliferation or cell differentiation or which may induce
CC      production of other cytokines in other cell populations. The
CC      polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC      peptide therapy. The polypeptides have various cytokine-like activities,
CC      e.g. stem cell growth factor activity, haematopoiesis regulating
CC      activity, tissue growth factor activity, immunomodulatory activity and
CC      activin/inhibin activity and may be useful in the diagnosis and/or
CC      treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC      inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC      (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC      sequence listing were missing at the time of publication
XX
SQ      Sequence 943 AA;

Query Match          94.5%; Score 4526.5; DB 4; Length 943;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 863; Conservative 2; Mismatches 10; Indels 67; Gaps 4;

Qy      1 MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP 60
        | ||| :| | |||||
Db      25 MTRRPSL-----MAGRQHGWSAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP 76

Qy      61 VLLVCKAVPATQIFFKCNGEVRQVDHVIERSTDGSSGLPTMEVRINVSRQQVEKVFGLE 120
        |||||
Db      77 VLLVCKAVPATQIFFKCNGEVRQVDHVIERSTDGSSGLPTMEVRINVSRQQVEKVFGLE 136

Qy      121 EYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPPEGIPPAE 180
        |||||
Db      137 EYWCQCVAWSSSGTTKSQKAYIRIAYLRKNFEQEPLAKEVSLEQGIVLPCRPPPEGIPPAE 196

Qy      181 VEWLNRNEDLVDPSLDPNVYITREHSLVVROARLADTANYTCVAKNIVARRRSASAAVIVY 240
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Db	197	VEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAIVIVY	256
Qy	241	-----VNGGWSTWTEWSVCSASCGRGWQKRSRSTN	271
Db	257	GGPRDSLVTGRGTAVPLGSDMWLSFSVRPVNGGWSTWTEWSVCSASCGRGWQKRSRSTN	316
Qy	272	PAPLNGGAFCEGQNVQKTACATLCPVDGSWSPWSKWSACGLDCTHWSRECSDPAPRNGG	331
Db	317	PAPLNGGAFCEGQNVQKTACATLCPVDGSWSPWSKWSACGLDCTHWSRECSDPAPRNGG	376
Qy	332	EECQGTDLDRNCTSDLCVH-----SASGPEDVALYVGLIAVAVCLVLLL	376
Db	377	EECQGTDLDRNCTSDLCVHNSYTPAPTAMLSPAAASGPEDVALYVGLIAVAVCLVLLL	436
Qy	377	LVLILVYCRKKEGLDSDVADSSILTSQFQVPSIKPSKADNPHLLTIQPDLSSTTTTYQGS	436
Db	437	LVLILVYCRKKEGLDSDVADSSILTSQFQVPSIKPSKADNPHLLTIQPDLSSTTTTYQGS	496
Qy	437	LCPRQDGSPKQFQLTNGHLLSPLGGGRHTLHHSSPTSEAEFVSRLSTQNYFRSLPRGTS	496
Db	497	LCPRQDGSPKQFQLTNGHLLSPLGGGRHTLHHSSPTSEAEFVSRLSTQNYFRSLPRGTS	556
Qy	497	NMTYGTFFNFGGRLMIPNTGISLLIPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTLLS	556
Db	557	NMTYGTFFNFGGRLMIPNTGISLLIPDAIPRGKIYEIYLTLHKPED-----	603
Qy	557	PIVSCGPPGVLLTRPVILAMDHCGEPSPDSSWLRLLKQSCGSEWEDVLHLGEEAPSHLYY	616
Db	604	--VSCGPPGVLLTRPVILAMDHCGEPSPDSSWLRLLKQSCGSEWEDVLHLGEEAPSHLYY	661
Qy	617	CQLEASACYVFTEQLGRFALVGEALSVAALKRLKLLLFAPVACTSLEYNIRVYCLHDTHD	676
Db	662	CQLEASACYVFTEQLGRFALVGEALSVAALKRLKLLLFAPVACTSLEYNIRVYCLHDTHD	721
Qy	677	ALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSSLWKSCLLVSYQEIPFYHI	736
Db	722	ALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSSLWKSCLLVSYQEIPFYHI	781
Qy	737	WNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINFNITKDTREAEALLAES	796
Db	782	WNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINFNITKDTREAEALLAES	841
Qy	797	EAGVPALVGPSAFKIPFLIRQKIISLDPCCRRGADWRTLAQKLHLDHLSFFASKPSPT	856
Db	842	EAGVPALVGPSAFKIPFLIRQKIISLDPCCRRGADWRTLAQKLHLDHLSFFASKPSPT	901
Qy	857	AMILNLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAE	898
Db	902	AMILNLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAE	943

RESULT 8

AAU74818

ID AAU74818 standard; protein; 842 AA.

XX

AC AAU74818;

XX
 DT 23-APR-2002 (first entry)
 XX
 DE Human REPTR 1 protein.
 XX
 KW REPTR; human; antiinflammatory; cytostatic; immunosuppressive; antiviral;
 KW anti-HIV; antiarthritic; anticonvulsant; nootropic; neuroprotective;
 KW antiallergic; antibody; immunogen; endometriosis;
 KW gastrointestinal disorder; gastritis; oesophageal carcinoma;
 KW Crohn's disease; irritable bowel syndrome; ulcerative colitis;
 KW endocrine disorder; hypothalamus disorder; Kallman's disease;
 KW autoimmune disease; inflammatory disease; infertility; receptor;
 KW acquired immune deficiency syndrome; AIDS; rheumatoid arthritis; allergy;
 KW osteoarthritis; diabetes mellitus; multiple sclerosis;
 KW systemic lupus erythematosus; cell proliferative disorder; cancer;
 KW developmental disorder; Duchenne muscular dystrophy;
 KW Becker muscular dystrophy; neurological disorder; epilepsy;
 KW Alzheimer's disease; Huntington's disease; reproductive disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200198354-A2.
 XX
 PD 27-DEC-2001.
 XX
 PF 21-JUN-2001; 2001WO-US019942.
 XX
 PR 21-JUN-2000; 2000US-0214027P.
 PR 25-AUG-2000; 2000US-0228045P.
 PR 12-DEC-2000; 2000US-0255104P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Griffin JA, Kallick DA, Tribouley CM, Yue H, Nguyen DB, Tang YT;
 PI Lal P, Policky JL, Azimzai Y, Lu DAM, Graul R, Yao MG, Burford N;
 PI Hafalia AJA, Baughn MR, Bandman O, Patterson C, Yang J, Xu Y;
 PI Gandhi AR, Warren BA, Ding L, Sanjanwala MS, Duggan BM, Lu Y;
 XX
 DR WPI; 2002-090432/12.
 DR N-PSDB; ABK15169.
 XX
 PT Twelve human receptors (referred to as REPTR-1 to REPTR-12), useful in
 PT the diagnosis, treatment and prevention of gastrointestinal (e.g.
 PT gastritis), autoimmune/inflammatory (e.g. osteoarthritis) and cell
 PT proliferative (e.g. cancer) disorders.
 XX
 PS Claim 45; Page 111-113; 157pp; English.
 XX
 CC This invention relates to twelve human receptors cDNA sequences referred
 CC to as REPTR-1 to REPTR-12), and the proteins encoded thereby. The
 CC proteins of the invention may have antiinflammatory, cytostatic,
 CC immunosuppressive, antiviral, anti-HIV, antiarthritic, muscular active
 CC general, anticonvulsant, nootropic, neuroprotective, antiallergic
 CC activities. The sequences of the invention may be used to produce REPTR
 CC agonists or antagonists, and the protein sequences may be used to raise
 CC anti-REPTR antibodies. These molecules and the REPTR polynucleotides and
 CC polypeptides of the invention are useful in the diagnosis, treatment and

CC prevention of gastrointestinal (e.g. gastritis, oesophageal carcinoma,
 CC Crohn's disease, irritable bowel syndrome, ulcerative colitis), endocrine
 CC (e.g. hypothalamus disorder, Kallman's disease), autoimmune/ inflammatory
 CC (e.g. acquired immune deficiency syndrome (AIDS), rheumatoid arthritis,
 CC allergies, osteoarthritis, diabetes mellitus, multiple sclerosis,
 CC systemic lupus erythematosus), cell proliferative (e.g. cancer),
 CC developmental (e.g. Duchenne and Becker muscular dystrophy), neurological
 CC (e.g. epilepsy, Alzheimer's disease, Huntington's disease) and
 CC reproductive (e.g. infertility, endometriosis) disorders. Numerous other
 CC examples of each disorder are given in the specification. The present
 CC sequence represents the human REPTR1 protein sequence of the invention
 XX
 SQ Sequence 842 AA;

Query Match 92.1%; Score 4413; DB 5; Length 842;
 Best Local Similarity 93.5%; Pred. No. 0;
 Matches 840; Conservative 1; Mismatches 1; Indels 56; Gaps 1;

Qy	1	MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP	60
Db	1	MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP	60
Qy	61	VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQVEKVFGL	120
Db	61	VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQVEKVFGL	120
Qy	121	EYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPEGIPPAE	180
Db	121	EYWCQCVAWSSSGTTKSQKAYIRIAYLRKNFEQEPLAKEVSLEQGIVLPCRPEGIPPAE	180
Qy	181	VEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAIVIVY	240
Db	181	VEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAIVIVY	240
Qy	241	VNGGWSTWTEWSVCSASCGRGWQKRSRSCCTNPAPLNGGAFCEGQNVQKTACATLCPVDGS	300
Db	241	-----VDGS	244
Qy	301	WSPWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDTNRCTSDLCVHSASGPEDVA	360
Db	245	WSPWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDTNRCTSDLCVHTASGPEDVA	304
Qy	361	LYVGLIAVAVCLVLLLLVLILVYCRKKEGLSDSDVADSSILTSQFQVPSIKPSKADNPHELL	420
Db	305	LYVGLIAVAVCLVLLLLVLILVYCRKKEGLSDSDVADSSILTSQFQVPSIKPSKADNPHELL	364
Qy	421	TIQPDLSSTTTTYQGSCLPRQDGPSPKFQLTNGHLLSPLGGGRHTLHHSSPTSEAEFEVS	480
Db	365	TIQPDLSSTTTTYQGSCLPRQDGPSPKFQLTNGHLLSPLGGGRHTLHHSSPTSEAEFEVS	424
Qy	481	RLSTQNYFRSLPRGTSNMTYGTGFNGLGGRLMIPNTGISLLIPPDAIPRGKIYEIYTLHK	540
Db	425	RLSTQNYFRSLPRGTSNMTYGTGFNGLGGRLMIPNTGISLLIPPDAIPRGKIYEIYTLHK	484
Qy	541	PEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDSSWLRLLKKQSCGESW	600
Db	485	PEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDSSWLRLLKKQSCGESW	544

Qy	601	EDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVAAAKRLKLLLFAPVACT	660
Db	545	EDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVAAAKRLKLLLFAPVACT	604
Qy	661	SLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRSLIHDPSSLW	720
Db	605	SLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRSLIHDPSSLW	664
Qy	721	KSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINF	780
Db	665	KSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINF	724
Qy	781	NITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISSLDPPCRRGADWRTLAQKL	840
Db	725	NITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISSLDPPCRRGADWRTLAQKL	784
Qy	841	HLDSHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAE	898
Db	785	HLDSHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAE	842

RESULT 9

AAW78899

ID AAW78899 standard; protein; 556 AA.

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AC AAW78899;

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DT 25-MAR-2003 (revised)

DT 21-DEC-1998 (first entry)

XX

DE Human UNC-5 homologue UNC5H-1.

XX

KW UNC-5; UNC5H-1; human; netrin receptor; cell migration; axon guidance;
 KW diagnosis; therapy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 7

FT /note= "encoded by TG"

FT Misc-difference 67

FT /note= "encoded by ATCT"

FT Misc-difference 256

FT /note= "encoded by GC"

FT Misc-difference 262

FT /note= "encoded by TG"

FT Misc-difference 360

FT /note= "encoded by AG"

FT Misc-difference 367

FT /note= "encoded by CC"

FT Misc-difference 370

FT /note= "encoded by TC"

FT Misc-difference 542

FT /note= "encoded by GG"

XX

PN W09837085-A1.

XX
PD 27-AUG-1998.
XX
PF 19-FEB-1998; 98WO-US003143.
XX
PR 19-FEB-1997; 97US-00808982.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Tessier-Lavigne M, Leonardo ED, Hinck L, Masu M, Keinomasu K;
XX
DR WPI; 1998-495364/42.
DR N-PSDB; AAW78899.
XX
PT Netrin-binding, vertebrate proteins - useful for diagnosis, therapy and
PT the biopharmaceutical industry.
XX
PS Claim 1; Page 22-23; 32pp; English.
XX
CC UNC5H-1 and UNC5H-2 (see AAW78901) are human homologues of Caenorhabditis
CC elegans UNC-5 protein. Their amino acid sequences were deduced from
CC isolated unc5h cDNA clones (see AAV52941 and AAV52943) isolated from an
CC embryonic brain cDNA library. The predicted proteins show similarity with
CC UNC-5, possess 2 predicted Ig-like domains and 2 predicted thrombospondin
CC type-1 repeats, a predicted membrane spanning region, and a large
CC intracellular domain. They are predicted to be involved in cell migration
CC and axon guidance, and are characterised as receptor proteins for
CC netrins. Rat UNC5H-1 (see AAW78898) and UNC5H-2 (see AAW78900) proteins
CC are also claimed. Vertebrate UNC-5 proteins may be produced recombinantly
CC from transfected host cells. The invention also provides unc-5
CC hybridisation probes and primers, vertebrate UNC-5-specific binding
CC agents such as specific antibodies, and methods of making and using the
CC subject compositions in diagnosis (e.g. genetic hybridisation screens for
CC vertebrate unc-5 transcripts), therapy (e.g. gene therapy to modulate
CC vertebrate unc-5 gene expression) and in the biopharmaceutical industry
CC (e.g. as immunogens, reagents for modulating cell guidance, reagents for
CC screening chemical libraries for lead pharmacological agents, etc.).
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 556 AA;

Query Match 58.8%; Score 2815; DB 2; Length 556;
Best Local Similarity 96.9%; Pred. No. 1.2e-225;
Matches 539; Conservative 1; Mismatches 16; Indels 0; Gaps 0;

Qy	343	NCTSDLCVHSASGPEDVALYVGLIAVAVCLVLLLLVLILVYCRKKEGLDSDVADSSILTS	402
		:	
Db	1	NCTSDLXVHTASGPEDVALYVGLIAVAVCLVLLLLVLILVYCRKKEGLDSDVADSSILTS	60
Qy	403	GFQPVSIKPSKADNPHLLTIQPDLSSTTTTYQGS LCPRQDGSPK FQLTNGHLLSPLGGG	462
Db	61	GFQPVSIKPSKADNPHLLTIQPDLSSTTTTYQGS LCPRQDGSPK FQLTNGHLLSPLGGG	120
Qy	463	RHTLHHSSPTSEAEFVSRLSTQNYFRSLPRGTSNMTYGT FNFLGGRLMIPNTGISLLIP	522
Db	121	RHTLHHSSPTSEAEFVSRLSTQNYFRSLPRGTSNMTYGT FNFLGGRLMIPNTGISLLIP	180

Qy	523	PDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHC	582
Db	181	PDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHC	240
Qy	583	SPDSWSLRLKKQSCEGSWEDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALS	642
Db	241	SPDSWSLALKKQSCEGSWEDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALS	300
Qy	643	VAAAKRLKLLLFAPVACTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFK	702
Db	301	VAAAKRLKLLLFAPVACTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHLX	360
Qy	703	DSYHNLRLSIHDPSSLWKSLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLAC	762
Db	361	DSYHNLXLSXHDVPSSLWKSLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLAC	420
Qy	763	KLWVWQVEGDGQSFSINFNITKDTREFAELLALESEAGVPALVGPSAFKIPFLIRQKIIS	822
Db	421	KLWVWQVEGDGQSFSINFNITKDTREFAELLALESEAGVPALVGPSAFKIPFLIRQKIIS	480
Qy	823	LDPPCRRGADWRTLAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAG	882
Db	481	LDPPCRRGADWRTLAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAG	540
Qy	883	LGQPDAGLFTVSEAE	898
Db	541	TPAGRWLLSQCEAE	556

RESULT 10

AAB50691

ID AAB50691 standard; protein; 931 AA.

XX

AC AAB50691;

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DT 19-MAR-2001 (first entry)

XX

DE Human UNC5C protein SEQ ID NO:90.

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KW Human; Caenorhabditis elegans; UNC-5; splice variant; nematode worm;
 KW protein-protein interaction; identification.

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OS Homo sapiens.

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PN WO200073328-A2.

XX

PD 07-DEC-2000.

XX

PF 02-JUN-2000; 2000WO-EP005108.

XX

PR 01-JUN-1999; 99GB-00012755.

XX

PA (DEVG-) DEVG NV.

XX

PI Van Criekinge W, Roelens I, Bogaert T, Verwaerde P;

XX

DR WPI; 2001-016508/02.

Db	441	DLTSAAMYRGVPVYALHD-VSDKIPMTNSPILDPLPNLKIKVYNTSGAVSPQDDLSEFTS	499
Qy	481	RLS---TQNYF-----RSLPRGT--SNMTYGTFNFLGGRLMIPNTGISLLIPDAI	526
Db	500	KLSPQMTQSLLENEALSLKNQSLARQTDPSCTAFGSFNSLGGHLIVPNSGVSLIPAGAI	559
Qy	527	PRGKIYEIYLTTLHKPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSDDS	586
Db	560	PQGRVYEMYVTVHRKETMRPPMDDSQTLTTPVVS CGPPGALLTRPVVLTMHHCADPNTED	619
Qy	587	WSLRLKKQSCEGSWEDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVA	646
Db	620	WKILLKNQAAQGWEDVVVGEENFTTPCYIKLDAEACHILTENLSTYALVGHSTTKAAA	679
Qy	647	KRLKLLLFAPVACTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYH	706
Db	680	KRLKLAIFGPLCCSSLEYSIRVYCLDDTDALKEILHLERQTGGQLLEEPKALHFKGSTH	739
Qy	707	NLRLSIHDPSSLWKSLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWV	766
Db	740	NLRLSIHDIASLWKSLLAKYQEIPFYHVWSGSQRNHCTFTLERFSLNTVELVCKLCV	799
Qy	767	WQVEGDGQSFSINFNITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISLDPP	826
Db	800	RQVEGEGQIFQLNCTVSEEPTGIDLPLLD PANTITVTGPSAFSIPLPIRQKLCSSLDAP	859
Qy	827	CRRGADWRTLAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAVAGLGQP	886
Db	860	QTRGHDWRMLAHKLNLD RYLN YFATKSSPTGVILDLWEAQNFDPGNLSMLAAVLEEMGRH	919
Qy	887	DAGLFTVSEAE	897
Db	920	ETVVSIAAEGQ	930

RESULT 11

ADE63098

ID ADE63098 standard; protein; 931 AA.

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AC ADE63098;

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DT 29-JAN-2004 (first entry)

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DE Human Protein AAC67491, SEQ ID NO 9033.

XX

KW Human; pain; neuronal tissue; gene therapy;

KW spinal segmental nerve injury; chronic constriction injury; CCI;

KW spared nerve injury; SNI; Chung.

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OS Homo sapiens.

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PN WO2003016475-A2.

XX

PD 27-FEB-2003.

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PF 14-AUG-2002; 2002WO-US025765.

XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; AAC67491.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
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PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 931 AA;

Query Match 57.5%; Score 2755; DB 7; Length 931;
Best Local Similarity 56.4%; Pred. No. 2.8e-220;
Matches 514; Conservative 154; Mismatches 215; Indels 28; Gaps 9;

Qy 9 PALLGIVLAAWLRGSGAQQS---ATVANPVPGANPDLLPHFLVEPEDVYIVKNKPVLLVC 65
||| :|:| ||| : | |:| ||||: ||: ||||| |||
Db 26 PAL--ALLSASGTGSAAQDDDFHELPETFPSPDPPEPLPHFLIEPEEAYIVKNKPVNLYC 83
Qy 66 KAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQVEKVFGLLEEYWCQ 125

Db	84	KASPATQIYFKCNSEWVHQKDHIVDERVDETSGLIVREVSIEISRQQVEELFGPEDYWCQ	143
Qy	126	CVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPEGIPPAEVEWLR	185
Db	144	CVAWSSAGTTKSRKAYVRIAYLRKTFEQEPLGKEVSLEQEVLLQCRPEGIPVAEVEWLK	203
Qy	186	NEDLVDPISLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAAVIVYVNGGW	245
Db	204	NEDIIDPVEDRNFYITIDHNLIIKQARLSDTANYTCVAKNIVAKRKSTTATVIVYVNGGW	263
Qy	246	STWTEWSVCSASCGRGWQKRSRSCNTPAPLNGGAFCEGQNVQKTACATLCPVDGWSWPWS	305
Db	264	STWTEWSVCNSRSCGRGYQKRTRCTNPAPLNGGAFCEGQSVQKIACCTLCPVDGRWTPWS	323
Qy	306	KWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDTNRNCTSDLCVHSASGPEDVALYVGL	365
Db	324	KWSTCGTECTHWRRECTAPAPKNGGKDCDGLVLQSKNCTDGLCMQTAPDSDDVALYVGI	383
Qy	366	-IAVAVCLVLLLLVLILVYCRKKEGLSDVDASSILTSGFQPVSIKPSKADNPHELLTIQP	424
Db	384	VIAVIVCLAISVVVALFVYRKNHRDFESDIIDSSALNGGFQPVNIKAARQD---LLAVPP	440
Qy	425	DLSTTTTTYQGSCLPRQDGPSPKFQLTNGHLLSPLGGGRHTLHHS-----SPTSEAEFEVS	480
Db	441	DLTSAAAMYRGPVYALHD-VSDKIPMTNSPILDPLPNLKIKVYNTSGAVSPQDDLSEFTS	499
Qy	481	RLS---TQNYF-----RSLPRGT--SNMTYGTNFNLGGRLMIPNTGISLLIPPDAI	526
Db	500	KLSPQMTQSLLENEALSLKNQSLARQTDPSCTAFGSFNSLGGHLIVPNSGVSLIIPAGAI	559
Qy	527	PRGKIYEIYLT LHKPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSDPS	586
Db	560	PQGRVYEMYVTVHRKETMRPPMDDSQTLLTPVVS CGPPGALLTRPVVLTMHHCADPNTED	619
Qy	587	WSLRLLKKQSCGWSWEDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVA	646
Db	620	WKILLKNQAAQGWEDVVVVGEENFTTPCYIKLDAEACHILTENLSTYALVGHSTTKAAA	679
Qy	647	KRLKLLLFAPVACTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYH	706
Db	680	KRLKLAIFGPLCCSSLEYSIRVYCLDDTQDALKEILHLERQTGGQLLEEPKALHFKGSTH	739
Qy	707	NLRLSIHDVPSSLWKSLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWV	766
Db	740	NLRLSIHDIAHSLWKSLLAKYQEIPFYHVWSGSQRNLHCTFTLERFSLNTVELVCKLCV	799
Qy	767	WQVEGDGQSFSINFNITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISSLDPP	826
Db	800	RQVEGEGQIFQLNCTVSEETPIDLPLLDPAANTITVTGPSAFSIPLPPIRQKLCSSLDAP	859
Qy	827	CRRGADWRTLAQKLHLDSHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQP	886
Db	860	QTRGHDWRMLAHKLNLDRLNYFATKSSPTGVILDLWEAQNFDPGNLSMLAAVLEEMGRH	919
Qy	887	DAGLFTVSEAE	897

RESULT 12

ABG11551

ID ABG11551 standard; protein; 982 AA.

XX

AC ABG11551;

XX

DT 18-FEB-2002 (first entry)

XX

DE Novel human diagnostic protein #11542.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

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OS Homo sapiens.

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PN WO200175067-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US008631.

XX

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Drmanac RT, Liu C, Tang YT;

XX

DR WPI; 2001-639362/73.

DR N-PSDB; AAS75738.

XX

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX

PS Claim 20; SEQ ID NO 41910; 103pp; English.

XX

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 982 AA;

Query Match 57.5%; Score 2755; DB 4; Length 982;
Best Local Similarity 56.4%; Pred. No. 3e-220;
Matches 514; Conservative 154; Mismatches 215; Indels 28; Gaps 9;

Qy 9 PALLGIVLAAWLRGSGAQQS---ATVANFPVPGANPDLLPHFLVEPEDVYIVKNKPVLLVC 65
||| :||| ||| : | | : |||||:||||: ||||| | |
Db 77 PAL--ALLSASGTGSAAQDDDFHELPETFPSPDPEPLPHFLIEPEEAYIVKNKPVNLYC 134

Qy 66 KAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQVEKVFGLLEEYWCQ 125
|| |||||:|||| ||| | ||::: | :||| || | :|||||:||| | :||| |
Db 135 KASPATQIYFKCNSEWVHQKDHIVDERVDETSGLIVREVSIEISRQVEELFGPEDYWCQ 194

Qy 126 CVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPGEGIPPAEVEWLRL 185
|||||:|||||:||||: ||| ||||| ||||| :|| ||||| ||||| :
Db 195 CVAWSSAGTTKSRKAYVRIAYLRKTFEQEPLGKEVSLEQEVLLQCRPPGEGIPVAEVEWLK 254

Qy 186 NEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAAVIVYVNGGW 245
|||: ||| | | ||| :||: ||: |||||: |||||: |||||: ||| :| ||||| |
Db 255 NEDIIDPVEDRNFYITIDHNLIIKQARLSDTANYTCVAKNIVAKRKSTTATVIVYVNGGW 314

Qy 246 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACATLCPVDGWSWPWS 305
|||||||: ||||: ||||: ||||: |||||: |||||: |||||: ||||| :||| |
Db 315 STWTEWSVCNSRCGRGYQKRTRCTNPAPLNGGAFCEGQSVQKIACITLCPVDGRWTPWS 374

Qy 306 KWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDTNRNCTSDLCVHSASGPEDVALYVGL 365
||| || :||| ||| : |||: |||: ||| : | | : ||| ||| : | : ||||| :
Db 375 KWSTCGTECTHWRRECTAPAPKNGGKDCDGLVLQSKNCTDGLCMQTAPDSDDVALYVGI 434

Qy 366 -IAVAVCLVLLLLVLILVYCRKKEGLDSDVADSSILTSGFQPVSIKPSKADNPHLLTIQP 424
||| ||| : :|| : || : :||: ||| | ||||: || :| || : |
Db 435 VIAVIVCLAISVVVALFVYRKNHRDFESDIIDSSALNGGFQPVNIKAARQD---LLAVPP 491

Qy 425 DLSTTTTTYQGLCPRQDGPSPKFQLTNGHLLSPLGGGRHTLHHS----SPTSEAEFEVS 480
||: : ||: | | | :|| : || | : :|| : ||| : |||
Db 492 DLTSAAMYRGVPVYALHD-VSDKIPMTNSPILDPLPNLKI K VYNTSGAVSPQDDLSEFTS 550

Qy 481 RLS---TQNYF-----RSLPRGT--SNMTYGTNFGGRLMIPNTGISLLIPPDAI 526
:|| ||: :|| | | | :||: ||| | :||: ||| ||
Db 551 KLSPQMTQSLLENEALSLKNQSLARQTDPSCTAFGSFNSLGGHLIVPNSGVSLIPAGAI 610

Qy 527 PRGKIYEIYLT LHKPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPPSDS 586
| :||: ||: ||: | :| | : |||: ||: ||||| |||||: | | | :|| :
Db 611 PQGRVYEMYVTVHRKETMRPPMDDSQTLLTPVVS CGPPGALLTRPVVLTMHHCADPNTED 670

Qy 587 WSLRLKKQSCEGSWEDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVA 646
| : || | : :| ||||: ||| : | :||: ||| : ||| : : |||
Db 671 WKILLKNQAAQGWEDVVVVGEENFTTPCYIKLDAEACHILTENLSTYALVGHSTTKAAA 730

Qy 647 KRLKLLLFAPVACTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYH 706

Db	731	KRLKLAIFGPLCCSSLEYSIRVYCLDDTQDALKEILHLERQTGGQLLEEPKALHFKGSTH	790
Qy	707	NLRLSIHDPSSLWKSLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWV	766
Db	791	NLRLSIHDIAHSLWKSLLAKYQEIPFYHVWSGSQRNHCTFTLERFSLNTVELVCKLCV	850
Qy	767	WQVEGDGQSFSINFNITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISSLDPP	826
Db	851	RQVEGEGQIFQLNCTVSEETGIDLPLLDPANTITTVTGPSAFSIPLPPIRQKLCSSLDAP	910
Qy	827	CRRGADWRTLAQKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQP	886
Db	911	QTRGHDWRMLAHKLNLDryLNYFATKSSPTGVILDLWEAQNFDPGNLSMLAAVLEEMGRH	970
Qy	887	DAGLFTVSEAE	897
Db	971	ETVVSLLAEGQ	981

RESULT 13

ADE63096

ID ADE63096 standard; protein; 945 AA.

XX

AC ADE63096;

XX

DT 29-JAN-2004 (first entry)

XX

DE Rat Protein AAB57679, SEQ ID NO 9031.

XX

KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX

OS Rattus norvegicus.

XX

PN WO2003016475-A2.

XX

PD 27-FEB-2003.

XX

PF 14-AUG-2002; 2002WO-US025765.

XX

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX

PA (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX

PI Woolf C, D'urso D, Befort K, Costigan M;

XX

DR WPI; 2003-268312/26.

DR GENBANK; AAB57679.

XX

PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.

XX

PS Claim 1; Page; 1017pp; English.

XX

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 945 AA;

Query Match 53.8%; Score 2578.5; DB 7; Length 945;
Best Local Similarity 53.0%; Pred. No. 1.5e-205;
Matches 509; Conservative 142; Mismatches 231; Indels 79; Gaps 17;

Qy 1 MAVRPGLWPALLGIVLAAW-----LRG--SGAQQSATVANPVPGANPDLLPHFLVEPEDV 53
| | | | | : | | | | | : : | | : | | | : | | |
Db 1 MRARSGARGALLLALLLCWDPTPSLAGIDSGGQ---ALPDSFSPAPAEQLPHFLLEPEDA 57

Qy 54 YIVKNKPVLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRQQV 113
| | | | | | | | | | | : | | | | | : | | | | | | | | | | | | | | | | | |
Db 58 YIVKNKPVLELHCRAFPATQIYFKCNGEWVSQKGHVTQESLDEATGLRIREVQIEVSRQQV 117

Qy 114 EKVFGLLEEYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPP 173
| : | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 118 EELFGLLEDYWCQCVAWSSSGTTKSRRAYIRIAYLRKNFDQEPLAKEVPLDHEVLLQCRPP 177

Qy 174 EGIPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSA 233
| | : | | | | | : | | : | | | : | | : | | : | | : | | : | | : | | : | |
Db 178 EGVPAEVEWLKNEVDIDPAQDTNFLTIDHNLIIRQARLSDTANYTCVAKNIVAKRRST 237

Qy 234 SAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRCTNPAPLNGGAFCEGQNVQKTACAT 293
: | | | | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 238 TATVIVYVNGGWSSWAEWSPCSNRCGRGWQKRTRCTNPAPLNGGAFCEGQACQKTACTT 297

Qy 294 LCPVDGSWSPWSKWSACGLDCTHWSRECS DPAPRNGGEECQGTDLDRNCTSDLCV--- 350
: | | | | : | : | | | | | : | | | | | | | | | | | | | | | | | | | | | |

XX
 KW UNC-5; UNC5H-2; rat; netrin receptor; cell migration; axon guidance;
 KW diagnosis; therapy.
 XX
 OS Rattus sp.
 XX
 FH Key Location/Qualifiers
 FT Peptide 148. .161
 FT /note= "peptide used to raise rabbit polyclonal antisera"
 FT Misc-difference 753
 FT /note= "encoded by CG"
 FT Peptide 909. .924
 FT /note= "peptide used to raise rabbit polyclonal antisera"
 XX
 PN WO9837085-A1.
 XX
 PD 27-AUG-1998.
 XX
 PF 19-FEB-1998; 98WO-US003143.
 XX
 PR 19-FEB-1997; 97US-00808982.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Tessier-Lavigne M, Leonardo ED, Hinck L, Masu M, Keinomasu K;
 XX
 DR WPI; 1998-495364/42.
 DR N-PSDB; AAV52942.
 XX
 PT Netrin-binding, vertebrate proteins - useful for diagnosis, therapy and
 PT the biopharmaceutical industry.
 XX
 PS Claim 1; Page 24-26; 32pp; English.
 XX
 CC UNC5H-1 and UNC5H-2 (see AAW78900) are rat homologues of Caenorhabditis
 CC elegans UNC-5 protein. Their amino acid sequences were deduced from
 CC isolated unc5h cDNA clones (see AAV52940 and AAV52942) isolated from an
 CC E18 brain cDNA library. The predicted proteins show similarity with UNC-
 CC 5, possess 2 predicted Ig-like domains and 2 predicted thrombospondin
 CC type-1 repeats, a predicted membrane spanning region, and a large
 CC intracellular domain. They are predicted to be involved in cell migration
 CC and axon guidance, and are characterised as receptor proteins for
 CC netrins. Human UNC5H-1 (see AAW78899) and UNC5H-2 (see AAW78901) proteins
 CC are also claimed. Vertebrate UNC-5 proteins may be produced recombinantly
 CC from transfected host cells. The invention also provides unc-5
 CC hybridisation probes and primers, vertebrate UNC-5-specific binding
 CC agents such as specific antibodies, and methods of making and using the
 CC subject compositions in diagnosis (e.g. genetic hybridisation screens for
 CC vertebrate unc-5 transcripts), therapy (e.g. gene therapy to modulate
 CC vertebrate unc-5 gene expression) and in the biopharmaceutical industry
 CC (e.g. as immunogens, reagents for modulating cell guidance, reagents for
 CC screening chemical libraries for lead pharmacological agents, etc.).
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 943 AA;

Query Match

53.7%; Score 2571.5; DB 2; Length 943;

Best Local Similarity 53.3%; Pred. No. 5.8e-205;
Matches 504; Conservative 142; Mismatches 221; Indels 79; Gaps 16;

```
Qy      9 PALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKPVLLVCKAV 68
      |:| ||      ||| : : | | : ||||:|||| ||||| | |:|
Db     21 PSLAGI-----DSGAQ---GLPDSFSPAPAEQLPHFLLEPEDAYIVKNKPVLEHLCRAF 70

Qy     69 PATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRQQVEKVFGLLEEYWCQCVA 128
      ||||:||||| | || : | | :|| ||:| |||||:|:||||:|||||
Db     71 PATQIYFKCNGEWVSQKGHVTDQESLDEATGLRIREVQIEVSRQQVEELFGLEDYWCQCVA 130

Qy    129 WSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPGIPPAEVEWLRNED 188
      |||||:|:|||| | |||:||||| |: :| ||||:| ||||:|
Db    131 WSSSGTTKSRRAYIRIAYLRKNFDQEPLAKEVPLDHEVLLQCRPPEGVPVAEVEWLKNE 190

Qy    189 LVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAAVIVYVNGGWSTW 248
      :||: | | :| :|:|:||||:||||| |||||:| ||| :| |||||:|
Db    191 VIDPAQDTNFLTIDHNLIRQARLSDTANYTCVAKNIVAKRRSTTATVIVYVNGGWSSW 250

Qy    249 TEWSVCSASCGRGWQKRSRCTNPAPLNGGAFCEGQNVQKTACATLCPVDGSWSPWSKWS 308
      ||| || |||||:|:||||| |||| |:||||:|: ||||
Db    251 AEWSPCSNRCGRGWQKRTRCTNPAPLNGGAFCEGQACQKTACTTVCPVDGAWTEWSKWS 310

Qy    309 ACGLDCTHWSRECSDPAPRNGGEECQGTDLDRNCTSDLCV---HSASGPE----- 357
      || :| ||||| | |:|| :| || |:| || || : : |:
Db    311 ACSTECAHWSRECMAPPQNGGRDCSGTLLDSKNCTDGLCVLNQRTLNDPKSRPLEPSG 370

Qy    358 DVALYVGL-IAVAVCLVLLLLVLILVYCRKKEGLDSDVADSS-ILTSGFQPVSIKPSKAD 415
      |||| || :|| | | :|: | :|| | |:| || || || |:| :|
Db    371 DVALYAGLVVAVFVVLAVLMAVGIVYRRNCRDFDITDSSAALTGGFHPVNFKTARPS 430

Qy    416 NPHLL--TIQPDLSSTTTTTYQGSCLPRQDGPSPKFQLTNGHLLSPL----- 459
      || || : : |||: : |:| : || : | :|| || ||
Db    431 NPQLLHPSAPPDLTASAGIYRGFVYALQDS-ADKIPMTNSPLLDPLPSLKIKVYDSSTIG 489

Qy    460 -GGG-----RHTLHHSSPTSEAEFVSRLSTQNYFRSLPRGT 495
      | |      | || | : | : | ||
Db    490 SGAGLADGADLLGVLPPGTYPGDFSRDTHFLHLS-----ASLGSQ-HLLGLPRDP 539

Qy    496 SNMTYGTNFNLGGRMIPNTGISLLIPPDAIPRGKIYEIYLTLHKPEDVRLPLA-GCQTL 554
      |: ||| |||| || |:|:| |||:| |:|:| :| | |||:| ||:
Db    540 SSSVSGTFGCLGGRLTIPGTGVSLVLPNGAIPQGFYDLYLRINKTEST-LPLSEGSQTV 598

Qy    555 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDPSWSLRLKKQSCGWSWEDVLHLGEEAPSHL 614
      ||| |:| || |:| |||:| : || | | :|| |:| |||:| || :
Db    599 LSPSVTCGPTGLLLCRPVVLTVPHCAEVIAGDWIFQLKTQAHQGHWEVVTLDEETLNT 658

Qy    615 YYCQLEASACYVFTEQLGRFALVGEALSVAANKRLKLLFAPVACTSLEYNIRVYCLHDT 674
      ||||| :|: : ||| : ||: | :| |||:| :|| |||||:| ||| ||
Db    659 CYCQLEAKSCHILLDQLGTYVFTGESYSRSVAVKRLQLAIFAPALCTSLEYSLRVYCLEDT 718

Qy    675 HDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRSLIHDVPSSLWKSKLLVSYQEIPFY 734
      |||||:|: ||| |:|:| | |||||:|:| : |:| || |||||
Db    719 PAALKEVLELERTLGGYLVEEPKTLLEFKDSYHNLRSLHDI PHAHWSKLLAKYQEIPFY 778

Qy    735 HIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINFNITKDTRFAELLAL 794
      |:|:|: ||||| | ::: ||: | |||:| | : : : | ||
```

Db 779 HVWNGSQKALHCTFTLERHSLASTEFTCKVCVRQVEGEGQIFQLHTTLA-ETPAGSLDAL 837
 Qy 795 ESEAGVPAL--VGPSAFKIPFLIRQKIISLDPPCRGGADWRTLAQKLHLDHLSFFASK 852
 | | | :|| |||| | ||| :|| | || ||| |||| :| :|::||:|
 Db 838 CSAPGNAATTQLGPYAFKIPLSIRQKICNSLDAPNSRGNDWRLLAQKLSMDRYLNYFATK 897
 Qy 853 PSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAEK 898
 ||| :||:|||| :||: ||:| :|: : : : : :|
 Db 898 ASPTGVILDLWEARQQDDGDLNSLASALEEMGKSEMLVAMTTDGDC 943

RESULT 15

AAO18734

ID AAO18734 standard; protein; 933 AA.

XX

AC AAO18734;

XX

DT 24-OCT-2002 (first entry)

XX

DE Human NOV1a protein.

XX

KW Human; NOVX; autoimmune disease; cancer; infection; inflammatory disease;
 KW storage disorder; muscle disorder; neurodegenerative disorder; nootropic;
 KW developmental defect; neuroprotective; antiparkinsonian; hypotensive;
 KW hypertensive; haemostatic; cardiact; antianginal; dermatological;
 KW immunosuppressive; antiinflammatory; virucide; antibacterial; anti-HIV;
 KW antiparasitic; antiallergic; antiasthmatic; antirheumatic; antiarthritic;
 KW vulnerary; anorectic; antidiabetic; immunomodulator; antipsoriatic;
 KW nephrotropic; kerolytic; antiulcer; cerebroprotective; anticonvulsant;
 KW antiinfertility; antimanic; antidepressant; metabolic; cytostatic;
 KW tranquilizer; analgesic.

XX

OS Homo sapiens.

XX

PN WO200257450-A2.

XX

PD 25-JUL-2002.

XX

PF 29-NOV-2001; 2001WO-US048922.

XX

PR 29-NOV-2000; 2000US-0253834P.

PR 30-NOV-2000; 2000US-0250926P.

PR 25-JAN-2001; 2001US-0264180P.

PR 20-AUG-2001; 2001US-0313656P.

PR 05-OCT-2001; 2001US-0327456P.

PR 28-NOV-2001; 2001US-00327456.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Edinger S, Macdougall JR, Millet I, Ellerman K, Stone DJ;
 PI Gerlach V, Grosse WM, Alsobrook JP, Lepley DM, Rieger D, Burgess CE;
 PI Casman SJ, Spytek KA, Boldog FL, Li L, Padigar M, Mishra V;
 PI Patturajan M, Shenoy S, Rastelli L, Tchernev VT, Vernet CAM;
 PI Zerhusen BD, Malyankar UM, Guo X, Miller CE, Gangolli EA;

XX

DR WPI; 2002-590741/63.

DR N-PSDB; ABT06279.

Db	538	GCLGGRLSIPGTGVSLVPNGAIPQGKFYEMYLLINKAEST-LPLSEGTQTVLSPSVTCG	596
Qy	563	PPGVLLTRPVILAMDHCGEPSPDWSLRLKKQSCGWSWEDVLHLGEEAPSHLYYCQLEAS	622
Db	597	PTGLLLCRPVILTMPHCAEVSARDWIFQLKTQAHQGHWEVVTLDEETLNTPCYCQLEPR	656
Qy	623	ACYVFTEQLGRFALVGEALSVAANKRLKLLFAPVACTSLEYNIRVYCLHDTHDALKEVV	682
Db	657	ACHILLDQLGTYVFTGESYSRSYSAVKRLQLAVFAPALCTSLEYSLRVYCLEDTPVALKEVL	716
Qy	683	QLEKQLGGQLIQEPRVLHFKDSYHNLRSLHDPVSSLWKSLLVSYQEIPFYHIWNGTQR	742
Db	717	ELERTLGGYLVVEPKPLMFKDSYHNLRSLHDLPHAHWSKLLAKYQEIPFYHIWSGSQK	776
Qy	743	YLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINFNITKDTRFAELIALESEAG--V	800
Db	777	ALHCTFTLERHSLASTELTCKICVRQVEGEGQIFQLHTTLA-ETPAGSLDTLCSAPGSTV	835
Qy	801	PALVGPSAFKIPFLIRQKIISSLDPPCRRGADWRTLAQKLHLDSHLSFFASKPSPTAMIL	860
Db	836	TTQLGPYAFKIPLSIRQKICNSLDAPNSRGNDWRMLAQKLSMDRYLNYFATKASPTGVIL	895
Qy	861	NLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAEC	898
Db	896	DLWEALQQDDGDLNSLASALEEMGKSEMLVAVATDGDC	933

Search completed: July 6, 2004, 14:33:27
Job time : 68 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 6, 2004, 14:32:16 ; Search time 23 Seconds
(without alignments)
2015.657 Million cell updates/sec

Title: US-10-624-932-2
Perfect score: 4791
Sequence: 1 MAVRPGLWPALLGIVLAAWL.....AVAGLGQPDAGLFTVSEAE 898

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	4638	96.8	898	2	US-08-808-982-5	Sequence 5, Appli
2	4638	96.8	898	3	US-09-306-902A-5	Sequence 5, Appli
3	2815.5	58.8	557	2	US-08-808-982-6	Sequence 6, Appli
4	2815.5	58.8	557	3	US-09-306-902A-6	Sequence 6, Appli
5	2571.5	53.7	943	2	US-08-808-982-7	Sequence 7, Appli
6	2571.5	53.7	943	3	US-09-306-902A-7	Sequence 7, Appli
7	296.5	6.2	1172	1	US-08-313-288B-19	Sequence 19, Appl
8	294	6.1	102	2	US-08-808-982-8	Sequence 8, Appli
9	294	6.1	102	3	US-09-306-902A-8	Sequence 8, Appli
10	268.5	5.6	239	5	PCT-US93-01652-1	Sequence 1, Appli
11	268.5	5.6	1170	1	US-08-313-288B-20	Sequence 20, Appl

12	249.5	5.2	441	3	US-08-985-526-3	Sequence 3, Appli
13	243	5.1	469	1	US-08-313-288B-15	Sequence 15, Appl
14	238	5.0	218	3	US-08-985-526-1	Sequence 1, Appli
15	234.5	4.9	1395	3	US-09-540-245A-15	Sequence 15, Appl
16	215	4.5	788	2	US-08-918-914-4	Sequence 4, Appli
17	210	4.4	1651	3	US-09-540-245A-18	Sequence 18, Appl
18	206.5	4.3	1381	3	US-09-540-245A-16	Sequence 16, Appl
19	200	4.2	1069	4	US-09-877-730-2	Sequence 2, Appli
20	200	4.2	1150	4	US-09-877-730-8	Sequence 8, Appli
21	199	4.2	1266	4	US-08-506-296B-4	Sequence 4, Appli
22	196	4.1	904	4	US-09-877-730-6	Sequence 6, Appli
23	196	4.1	985	4	US-09-877-730-10	Sequence 10, Appl
24	193	4.0	380	4	US-09-877-730-4	Sequence 4, Appli
25	186	3.9	1297	3	US-09-540-245A-17	Sequence 17, Appl
26	185	3.9	481	4	US-09-130-491-8	Sequence 8, Appli
27	175.5	3.7	905	4	US-09-369-364A-9	Sequence 9, Appli
28	172	3.6	837	4	US-09-122-126B-2	Sequence 2, Appli
29	172	3.6	837	4	US-09-634-286A-2	Sequence 2, Appli
30	170.5	3.6	1224	4	US-09-930-872-4	Sequence 4, Appli
31	167.5	3.5	757	4	US-09-963-791-24	Sequence 24, Appl
32	167.5	3.5	908	4	US-09-963-791-2	Sequence 2, Appli
33	163	3.4	1081	4	US-09-369-364A-17	Sequence 17, Appl
34	161	3.4	1501	2	US-08-447-464-3	Sequence 3, Appli
35	161	3.4	1501	2	US-08-716-679-3	Sequence 3, Appli
36	160	3.3	930	4	US-09-369-364A-2	Sequence 2, Appli
37	160	3.3	930	4	US-09-122-126B-15	Sequence 15, Appl
38	160	3.3	930	4	US-09-634-286A-15	Sequence 15, Appl
39	159.5	3.3	551	4	US-09-130-491-16	Sequence 16, Appl
40	159.5	3.3	727	4	US-09-445-023A-12	Sequence 12, Appl
41	159.5	3.3	997	4	US-09-369-364A-7	Sequence 7, Appli
42	159	3.3	518	4	US-09-369-364A-22	Sequence 22, Appl
43	158.5	3.3	1911	1	US-08-348-006B-5	Sequence 5, Appli
44	158.5	3.3	1911	2	US-08-800-825A-5	Sequence 5, Appli
45	158.5	3.3	1911	3	US-09-158-657-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-08-808-982-5

; Sequence 5, Application US/08808982

; Patent No. 5939271

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; APPLICANT: Leonardo, E. David

; APPLICANT: Hink, Lindsay

; APPLICANT: Masu, Masayuki

; APPLICANT: Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

```

;      ZIP: 94104
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/808,982
;      FILING DATE:
;      CLASSIFICATION: 530
;      ATTORNEY/AGENT INFORMATION:
;      NAME: OSMAN, RICHARD A
;      REGISTRATION NUMBER: 36,627
;      REFERENCE/DOCKET NUMBER: UC96-217
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (415) 343-4341
;      TELEFAX: (415) 343-4342
;      INFORMATION FOR SEQ ID NO: 5:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 898 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: not relevant
;      TOPOLOGY: not relevant
;      MOLECULE TYPE: peptide
US-08-808-982-5

```

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Query Match          96.8%; Score 4638; DB 2; Length 898;
Best Local Similarity 96.0%; Pred. No. 0;
Matches 862; Conservative 17; Mismatches 19; Indels 0; Gaps 0;

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```

Qy      1 MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP 60
        |||
Db      1 MAVRPGLWPVLLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP 60

Qy     61 VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRQQVEKVFGL 120
        |||
Db     61 VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDSSSGLPTMEVRINVSRQQVEKVFGL 120

Qy    121 EYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPEGIPPAE 180
        |||
Db    121 EYWCQCVAWSSSGTTKSQKAYIRIAYLRKNFEQEPLAKEVSLEQGIVLPCRPPEGIPPAE 180

Qy    181 VEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAIVIVY 240
        |||
Db    181 VEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSTSAIVIVY 240

Qy    241 VNGGWSTWTEWSVCSASCGRGWQKRSRSCNTPAPLNGGAFCEGQNVQKTACATLCPVDGS 300
        |||
Db    241 VNGGWSTWTEWSVCSASCGRGWQKRSRSCNTPAPLNGGAFCEGQNVQKTACATLCPVDGS 300

Qy    301 WSPWSKWSACGLDCTHWSRECS DPAPRNGGEECQGTDLDTNRCTSDLCVHSASGPEDVA 360
        || |||
Db    301 WSSWSKWSACGLDCTHWSRECS DPAPRNGGEECRGADLDTNRCTSDLCCLHTASCPEDVA 360

Qy    361 LYVGLIAVAVCLVLLLLVLILVYCRKKEGLDSDVADSSILTSQFQPVSIKPSKADNPHLL 420
        ||:|:|:|
Db    361 LYIGLVAVAVCLFLLLLALGLIYCRKKEGLDSDVADSSILTSQFQPVSIKPSKADNPHLL 420

```

Qy 421 TIQPDLSSTTTTYYQGSCLPRQDGPSPKFQLTNGHLLSPLGGGRHTLHHSSPTSEAEFVS 480
 |||||:|||||
 Db 421 TIQPDLSSTTTTYYQGSCLSRQDGPSPKFQLSNGHLLSPLGSGRHTLHHSSPTSEAEFVS 480
 Qy 481 RLSTQNYFRSLPRGTSNMTYGTNFNLGGRLMIPNTGISLLIPPDAIPRGKIYEIYTLHK 540
 |||||:|||||
 Db 481 RLSTQNYFRSLPRGTSNMAYGTNFNLGGRLMIPNTGISLLIPPDAIPRGKIYEIYTLHK 540
 Qy 541 PEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDWSLRLKKQSCGSW 600
 |||||:|||||
 Db 541 PEDVRLPLAGCQTLLSPVSCGPPGVLLTRPVILAMDHCGEPSPDWSLRLKKQSCGSW 600
 Qy 601 EDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVAARKRLKLLFAPVACT 660
 |||||:|||||
 Db 601 EDVLHLGEEAPSHLYYCQLEAGACYVFTEQLGRFALVGEALSVAATKRLRLLLFAPVACT 660
 Qy 661 SLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSSLW 720
 |||||:|||||
 Db 661 SLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSSLW 720
 Qy 721 KSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINF 780
 |||||:|||||:|||||:|||||:|||||
 Db 721 KSKLLVSYQEIPFYHIWNGTQQYLHCTFTLERINASTSDLACKVWVWQVEGDGQSFNINF 780
 Qy 781 NITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISSLDPPCRRGADWRTLAQKL 840
 |||||:|||||
 Db 781 NITKDTRFAELLALESEGGVPALVGPSAFKIPFLIRQKIIASLDPPCSRGAADWRTLAQKL 840
 Qy 841 HLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAE 898
 |||||:|||||
 Db 841 HLDShLSFFASKPSPTAMILNLWEARHFPNGNLGQLAAAVAGLGQPDAGLFTVSEAE 898

RESULT 2

US-09-306-902A-5

; Sequence 5, Application US/09306902A

; Patent No. 6277585

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; Leonardo, E. David

; Hink, Lindsay

; Masu, Masayuki

; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

```

;      SOFTWARE: PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/306,902A
;      FILING DATE: 07-May-1999
;      CLASSIFICATION: <Unknown>
;      ATTORNEY/AGENT INFORMATION:
;      NAME: OSMAN, RICHARD A
;      REGISTRATION NUMBER: 36,627
;      REFERENCE/DOCKET NUMBER: UC96-217
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (415) 343-4341
;      TELEFAX: (415) 343-4342
;      INFORMATION FOR SEQ ID NO: 5:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 898 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: not relevant
;      TOPOLOGY: not relevant
;      MOLECULE TYPE: peptide
;      SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-306-902A-5

```

```

Query Match          96.8%;  Score 4638;  DB 3;  Length 898;
Best Local Similarity 96.0%;  Pred. No. 0;
Matches 862;  Conservative 17;  Mismatches 19;  Indels 0;  Gaps 0;

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```

Qy      1 MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP 60
        |||||||
Db      1 MAVRPGLWPVLLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP 60

Qy     61 VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRQQVEKVFGL 120
        |||||||
Db     61 VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDSSSGLPTMEVRINVSRQQVEKVFGL 120

Qy    121 EYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPGEGIPPAE 180
        |||||||
Db    121 EYWCQCVAWSSSGTTKSQKAYIRIAYLRKNFEQEPLAKEVSLEQGIVLPCRPPGEGIPPAE 180

Qy    181 VEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAIVY 240
        |||||||
Db    181 VEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSTSAIVY 240

Qy    241 VNGGWSTWTEWSVCSASCGRGWQKRSRSCNTPAPLNGGAFCEGQNVQKTACATLCPVDGS 300
        |||||||
Db    241 VNGGWSTWTEWSVCSASCGRGWQKRSRSCNTPAPLNGGAFCEGQNVQKTACATLCPVDGS 300

Qy    301 WSPWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDRNCTSDLCVHSASGPEDVA 360
        || |||||||
Db    301 WSSWSKWSACGLDCTHWSRECSDPAPRNGGEECRGADLDRNCTSDLCVHSASGPEDVA 360

Qy    361 LYVGLIAVAVCLVLLLLLVLYCRKKEGLDSDVADSSILTSQFQPVSIKPSKADNPHLL 420
        ||:|||||
Db    361 LYIGLVAVAVCLFLLLLLALGLIYCRKKEGLDSDVADSSILTSQFQPVSIKPSKADNPHLL 420

Qy    421 TIQPDLSSTTTTYQGSCLPRQDGPSPKFQLTNGHLLSPLGGGRHTLHHSSPTSEAEFVS 480
        |||||||
Db    421 TIQPDLSSTTTTYQGSCLSRQDGPSPKFQLSNGHLLSPLGSGRHTLHHSSPTSEAEFVS 480

```

Qy 481 RLSTQNYFRSLPRGTSNMTYGTNFNLGGRLMIPNTGISLLIPPDAIPRGKIYEIYTLHK 540
 |||||
 Db 481 RLSTQNYFRSLPRGTSNMAYGTNFNLGGRLMIPNTGISLLIPPDAIPRGKIYEIYTLHK 540
 |||||
 Qy 541 PEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDWSLRLKKQSCEGSW 600
 |||||:|||||
 Db 541 PEDVRLPLAGCQTLLSPVVSCGPPGVLLTRPVILAMDHCGEPSPDWSLRLKKQSCEGSW 600
 |||||
 Qy 601 EDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVAARKRLKLLLFAPVACT 660
 |||||:||||| |||||
 Db 601 EDVLHLGEESPSHLYYCQLEAGACYVFTEQLGRFALVGEALSVAATKRLRLLLFAPVACT 660
 |||||
 Qy 661 SLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDPVSSLW 720
 |||||
 Db 661 SLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDPVSSLW 720
 |||||
 Qy 721 KSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINF 780
 |||||:|||||: |||||:|||||
 Db 721 KSKLLVSYQEIPFYHIWNGTQQYLHCTFTLERINASTSDLACKVWVWQVEGDGQSFNINF 780
 |||||
 Qy 781 NITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISSLDPPCRRGADWRTLAQKL 840
 |||||:|||||
 Db 781 NITKDTRFAELLALESEGGVPALVGPSAFKIPFLIRQKIIASLDPPCSRGAADWRTLAQKL 840
 |||||
 Qy 841 HLDSHLSFFASKPSPTAMILNLWEARHFPGNLSQLAAVAGLGQPDAGLFTVSEAEC 898
 |||||
 Db 841 HLDSHLSFFASKPSPTAMILNLWEARHFPGNLGQLAAVAGLGQPDAGLFTVSEAEC 898
 |||||

RESULT 3

US-08-808-982-6

; Sequence 6, Application US/08808982

; Patent No. 5939271

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; APPLICANT: Leonardo, E. David

; APPLICANT: Hink, Lindsay

; APPLICANT: Masu, Masayuki

; APPLICANT: Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/808,982

; FILING DATE:

```

; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-808-982-6

```

```

Query Match          58.8%; Score 2815.5; DB 2; Length 557;
Best Local Similarity 96.8%; Pred. No. 5.2e-259;
Matches 539; Conservative 2; Mismatches 15; Indels 1; Gaps 1;

```

```

Qy      343 NCTSDLCVHSASGPEDVALYVGLIAVAVCLVLLLLVLILVYCRKKEGLDSDVADSSILTS 402
        ||||| ||:||||||||||||||||||||||||||||||||||||||||||
Db      1 NCTSDLXVHTASGPEDVALYVGLIAVAVCLVLLLLVLILVYCRKKEGLDSDVADSSILTS 60

Qy      403 GFQPVSIKPSKADNPHLLTIQPDLSSTTTTYQGS LCPQDGPSPKFQLTNGHLLSPLGGG 462
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      61 GFQPVSIKPSKADNPHLLTIQPDLSSTTTTYQGS LCPQDGPSPKFQLTNGHLLSPLGGG 120

Qy      463 RHTLHHSSPTSEAEFVSRLSTQNYFRSLPRGTSNMTYGT FNFLGGRLMIPNTGISLLIP 522
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      121 RHTLHHSSPTSEAEFVSRLSTQNYFRSLPRGTSNMTYGT FNFLGGRLMIPNTGISLLIP 180

Qy      523 PDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGE 582
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      181 PDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGE 240

Qy      583 SPDSWSLRLKKQSCEGSWEDVLHLGEEAPSHLYYCQLEASAC YVFTEQLGRFALVGEALS 642
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      241 SPDSWSLALKKQSCEGSWEDVLHLGEEAPSHLYYCQLEASAC YVFTEQLGRFALVGEALS 300

Qy      643 VAAAKRLKLLLFAPVACTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFK 702
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      301 VAAAKRLKLLLFAPVACTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHLX 360

Qy      703 DSYHNLRLSIHDVPSSLWKSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLAC 762
        ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      361 DSYHNLXLXHDVPSSLWKSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLAC 420

Qy      763 KLWVWQVEGDGQSFSINFNITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIIS 822
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      421 KLWVWQVEGDGQSFSINFNITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIIS 480

Qy      823 LDPPCRRGADWRTL AQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAG 882
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      481 LDPPCRRGADWRTL AQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAG 540

```


Qy 883 LGQPDAGLFT-VSEAEC 898
| : |||||
Db 541 TXPAGRWLLSQCSEAEC 557

RESULT 4

US-09-306-902A-6

; Sequence 6, Application US/09306902A

; Patent No. 6277585

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; Leonardo, E. David

; Hink, Lindsay

; Masu, Masayuki

; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/306,902A

; FILING DATE: 07-May-1999

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: OSMAN, RICHARD A

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: UC96-217

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 343-4341

; TELEFAX: (415) 343-4342

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 557 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: not relevant

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-306-902A-6

Query Match 58.8%; Score 2815.5; DB 3; Length 557;

Best Local Similarity 96.8%; Pred. No. 5.2e-259;

Matches 539; Conservative 2; Mismatches 15; Indels 1; Gaps 1;

Qy 343 NCTSDLCVHSASGPEDVALYVGLIAVAVCLVLLLLVLILVYCRKKEGLSDVDADSSILTS 402

||||| ||:|||||||||||||||||||||||||||||||||||||

Db 1 NCTSDLXVHTASGPEDVALYVGLIAVAVCLVLLLLVLILVYCRKKEGLSDVDADSSILTS 60


```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 943 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-808-982-7

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Query Match          53.7%; Score 2571.5; DB 2; Length 943;
Best Local Similarity 53.3%; Pred. No. 2.2e-235;
Matches 504; Conservative 142; Mismatches 221; Indels 79; Gaps 16;

```

```

Qy      9 PALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKPVLLVCKAV 68
      |:| ||      ||| : : | | : ||||:|||| ||||| | |:|
Db     21 PSLAGI-----DSGAQ---GLPDSFSPAPAEQLPHFLLEPEDAYIVKNKPVLEHCRAF 70

Qy     69 PATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRQQVEKVFGLLEEYWCQCVA 128
      ||||:||||| | | | : | | :|| | |:| |||||:||||:|||||
Db     71 PATQIYFKCNGEWVSQKGHVTQESLDEATGLRIREVQIEVSRQQVEELFGLEDYWCQCVA 130

Qy    129 WSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPGEGIPPAEVEWLRNED 188
      |||||:||||| ||||:||||| | : :| ||||:| ||||:|
Db    131 WSSSGTTKSRRAYIRIAYLRKNFDQEPLAKEVPLDHEVLLQCRPPEGVPVAEVEWLKNE 190

Qy    189 LVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAAVIVYVNGGWSTW 248
      ::||: | | : | :|:||||:|||||:|||||:| | |||||:|
Db    191 VIDPAQDTNFLTIDHNLIRQARLSDTANYTCVAKNIVAKRRSTTATVIVYVNGGWSSW 250

Qy    249 TEWSVCSASCGRGWQKRSRSCNTPAPLNGGAFCEGQNVQKTACATLCPVDGSWSPWSKWS 308
      ||| || |||||:|:||||| |||| |:||||:|: ||||
Db    251 AEWSPCSNRCGRGWQKRTRCTNPAPLNGGAFCEGQACQKTACTTVCPVDGAWTEWSKWS 310

Qy    309 ACGLDCTHWSRECSDPAPRNGGEECQGTDLDTNRCTSDLCV---HSASGPE----- 357
      || :| ||||| | |:|| :| || |:||| ||| : : | :
Db    311 ACSTECAHWSRECMAPPQNGGRDCSGTLLDSKNCTDGLCVLNQRTLNDPKSRPLEPSG 370

Qy    358 DVALYVGL-IAVAVCLVLLLLVLILVYCRKKEGLDSDVADSS-ILTSGFQPVSIKPSKAD 415
      |||| | | :| | | :| | :|| | |:| ||| || || |:| :
Db    371 DVALYAGLVVAVFVVLAVLMAVGIVYRRNCRDFDTDITDSSAALTGGFHPVNFKTARPS 430

```

Qy 416 NPHLL--TIQPDLSSTTTTYYQGSICPRQDGSPKQFQLTNGHLLSPL----- 459
 || || : ||| : : || : || : || || ||
 Db 431 NPQLLHPSAPDLTASAGIYRGFVYALQDS-ADKIPMTNSPLLDPLPSLKIKVYDSSTIG 489
 Qy 460 -GGG-----RHTLHHSSPTSEAEFVSRLSTQNYFRSLPRGT 495
 || | || | : || : ||
 Db 490 SGAGLADGADLLGVLPPGTYPGDFSRDTHFLHLRS-----ASLGSQ-HLLGLPRDP 539
 Qy 496 SNMTYGTFFNLGGRLMIPNTGISLLIPDAIPRGKIYEIYLT LHKPEDVRLPLA-GCQTL 554
 |: ||| |||| || ||:|||| |||: || |: || :| |||: | ||:
 Db 540 SSSVSGTFGCLGGRLTIPGTGVSLLVNGAIPQKGYDLYLRINKTEST-LPLSEGSQTV 598
 Qy 555 LSPIVSCGPPGVLLTRPVILAMDHCGEPSPDSSWLRKKQSCEGSWEDVLHLGEEAPSHL 614
 ||| |: ||| |: || |||: | : || | : || |: || : || :
 Db 599 LSPSVTCGPTGLLLCRPVVLTVP HCAEVIAGDWIFQLKTQAHQGHWEVVTLDEETLNT 658
 Qy 615 YYCQLEASACYVFTEQLGRFALVGEALSVAARKLKL LFPVACTSLEYNIRVYCLHDT 674
 ||||| :||: :||| : ||: | :| |||: | :|| | |||||: ||||| ||
 Db 659 CYCQLEAKSCHILLDQLGTYVFTGESYSRSYAVKRLQLAIFAPALCTSLEYSLRVYCLED 718
 Qy 675 HDALKEVVQLEKQLGGQLIQEPVRLHFKDSYHNLRSLIHDVPSSLWKSLLVSYQEIPFY 734
 |||||: ||: ||| |: ||: | ||||| |||||: ||: | : |||| | |||||
 Db 719 PAALKEVLELERTLGGYLVEEPKTL LFKDSYHNLRSLHDI PHAHWRSKLLAKYQEIPFY 778
 Qy 735 HIWNGTQRYLHCTFTLERVSPSTSD LACKLWVWQVEGDGQSFSINFNITKDTRFAELLAL 794
 |: |||: |: ||||| ||| :||: ||: | ||||: ||| :| : : | ||
 Db 779 HVWNGSQKALHCTFTLERHSLASTEFTCKVCVRQVEGEGQIFQLHTTLA-ETPAGSLDAL 837
 Qy 795 ESEAGVPAL--VGPSAFKIPFLIRQKIISSLDPPCRRGADWRTLAQKLHLD SHLSFFASK 852
 | | | :|| |||| | |||| :||| | || ||| |||| :| :||: ||:
 Db 838 CSAPGNAATTQLGPYAFKIPLSIRQKICNSLDAPNSRGNDWRLLA QKLSMDRYLNYFATK 897
 Qy 853 PSPTAMILNLWEARHFPNGNLSQLAAVAGLGQPDAGLFTVSEAEC 898
 ||| :||: |||| | :||: ||: ||: ||: : : : : :
 Db 898 ASPTGVILDLWEARQQDDGDLNSLASALEEMGKSEMLVAMTTDGDC 943

RESULT 6

US-09-306-902A-7

; Sequence 7, Application US/09306902A

; Patent No. 6277585

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; Leonardo, E. David

; Hink, Lindsay

; Masu, Masayuki

; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

```

;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/306,902A
;           FILING DATE: 07-May-1999
;           CLASSIFICATION: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
;           NAME: OSMAN, RICHARD A
;           REGISTRATION NUMBER: 36,627
;           REFERENCE/DOCKET NUMBER: UC96-217
;
; TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (415) 343-4341
;           TELEFAX: (415) 343-4342
;
; INFORMATION FOR SEQ ID NO: 7:
;           SEQUENCE CHARACTERISTICS:
;           LENGTH: 943 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: not relevant
;           TOPOLOGY: not relevant
;
;           MOLECULE TYPE: peptide
;           SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-306-902A-7

```

```

Query Match          53.7%;  Score 2571.5;  DB 3;  Length 943;
Best Local Similarity 53.3%;  Pred. No. 2.2e-235;
Matches 504;  Conservative 142;  Mismatches 221;  Indels 79;  Gaps 16;

```

```

Qy      9  PALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKPVLLVCKAV 68
        |:| ||      |||      : : | | : ||||:|||| ||||| ||| |:|
Db      21  PSLAGI-----DSGAQ---GLPDSFPSAPAEQLPHFLLEPEDAYIVKNKPVELHCRAF 70

Qy      69  PATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQQVEKVFGLLEEYWCQCVA 128
        ||||:||||||| | || : | | ::|| ||:| |||||::| |||:|||||
Db      71  PATQIYFKCNGEWVSQKGHVTQESLDEATGLRIREVQIEVSRQQVEELFGLLEDYWCQCVA 130

Qy      129  WSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLSEQGIVLPCRPPGIPPAEVEWLRNED 188
        |||||::| |||| | |||:||||||| | : ::| |||||:| |||||:|
Db      131  WSSSGTTKSRRAYIRIAYLRKNFDQEPLAKEVPLDHEVLLQCRPPEGVPVAEVEWLKNEED 190

Qy      189  LVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAAVIVYVNGGWSTW 248
        ::||: | | :| :|:|:||||:||||||| |||:| | |||||:|
Db      191  VIDPAQDTNFLTIDHNLIIRQARLSDTANYTCVAKNIVAKRRSTTATVIVYVNGGWSSW 250

Qy      249  TEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLCPVDGWSWSPWSKWS 308
        || | | |||||:|:||||||| |||| |:||||:|: ||||
Db      251  AEWSPCSNRCGRGWQKRTCTNPAPLNGGAFCEGQACQKTACTTVCPVDGAWTEWSKWS 310

Qy      309  ACGLDCTHWSRECSDPAPRNGGEECQGTDLDRNCTSDLCV---HSASGPE----- 357
        || :| ||||| | |:| | :| |||:| | || : : | :
Db      311  ACSTECAHWSRECMAPPPQNGGRDCSGTLLDSKNCTDGLCVLNQRTLNDPKSRPLEPSG 370

Qy      358  DVALYVGL-IAVAVCLVLLLLVLILVYCRKKEGLSDVADSS-ILTSGFQPVSIKPSKAD 415
        |||| | | :| | | :| :| | :| | | :| :| | | || | | :| :|
Db      371  DVALYAGLVVAVFVVLAVLMAVGVIVYRRNCRDFDTDITDSSAALTGGFHPVNFKTARPS 430

```

Qy 416 NPHLL--TIQPDLS'TTTTTYQGS LCP RQDGSPK FQLTNGHLLSPL----- 459
 || || : ||: : |: : || : | :|| || ||
 Db 431 NPQLLHPSAPPDLTASAGIYRGPVYALQDS-ADKIPMTNSPLLDPLPSLKIKVYDSSTIG 489
 Qy 460 -GGG-----RHTLHHSSPTSEAEFVSRLSTQNYFRSLPRGT 495
 | | | | | : | : | : ||
 Db 490 SGAGLADGADLLGVLPPGTYPGDFSRDTHFLHLRS-----ASLGSQ-HLLGLPRDP 539
 Qy 496 SNMTYGTFFNLGGRLMIPNTGISLLIPDAIPRGKIYEIYLT LHKPEDVRLPLA-GCQTL 554
 |: ||| |||| || ||: ||: | ||: || |: || :| | ||: | ||:
 Db 540 SSSVSGTFGCLGGRLTIPGTGVSLVPNGAIPQKGFDLYLRINKTEST-LPLSEGSQTV 598
 Qy 555 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCGWSWEDVLHLGEEAPSHL 614
 ||| |: ||| |: || ||: | : || | : || |: | ||: | || :
 Db 599 LSPSVTCGPTGLLLCRPVVLTVPHCAEVIAGDWIFQLKTQAHQGHWEVVTLDEETLNTP 658
 Qy 615 YYCQLEASACYVFTEQLGRFALVGEALSVA AAKRLKLLL FAPVACTSLEYNIRVYCLHDT 674
 ||||| :||: :||| : ||: | :| ||: | :|| | ||||: :||| ||
 Db 659 CYCQLEAKSCHILLDQLGTYVFTGESYSRSAVKRLQLAIFAPALCTSLEYS LRVYCLEDT 718
 Qy 675 HDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSSLWKS KLLVSYQEIPFY 734
 ||||: :||: ||| |: ||: | ||||| ||||: ||: | : |: ||| |||||
 Db 719 PAALKEVLELERTLGGYLVEEPKTL LFKDSYHNLRSLHDIPHAHWSKLLAKYQEIPFY 778
 Qy 735 HIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINFNITKDTRFAELLAL 794
 |: |||: |: ||||| | :||: ||: | ||||: || :| : :| | ||
 Db 779 HVWNGSQKALHCTFTLERHSLASTEFTCKVCVRQVEGEGQIFQLHTTLA-ETPAGSLDAL 837
 Qy 795 ESEAGVPAL--VGPSAFKIPFLIRQKIISSLDPPCRRGADWRTLAQKLHLDSHLSFFASK 852
 | | | :|| |||| |||| :||| | || || |||| :| :||: ||: |
 Db 838 CSAPGNAATTQLGPYAFKIPLSIRQKICNSLDAPNSRGNDWRLLAQKLSMDRYLNYFATK 897
 Qy 853 PSPTAMILNLWEARHFPGNLSQLAAAVAGLGQPDAGLFTVSEAEC 898
 ||| :||: |||| :||: ||: | :| : : : : :
 Db 898 ASPTGVILDLWEARQQDDGDLNSLASALEEMGKSEMLVAMTTDGDGDC 943

RESULT 7

US-08-313-288B-19

; Sequence 19, Application US/08313288B

; Patent No. 5750502

; GENERAL INFORMATION:

; APPLICANT: Jessell, Thomas M. and Avihu Klar

; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A

; TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

```

;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/313,288B
;   FILING DATE: January 5, 1995
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: White, John P.
;   REGISTRATION NUMBER: 28,678
;   REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 278-0400
;   TELEFAX: (212) 391-0526
;   TELEX:
;   INFORMATION FOR SEQ ID NO: 19:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1172 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-313-288B-19

```

```

Query Match          6.2%; Score 296.5; DB 1; Length 1172;
Best Local Similarity 30.5%; Pred. No. 1.4e-18;
Matches 78; Conservative 28; Mismatches 105; Indels 45; Gaps 9;

```

```

Qy      209 RQARLADTANYTCVAKNIVARRRSASAA-VIVYVNGGWSTWTEWSVCSASCGRGWQKRSR 267
        :: | | : ||: : | | | : : || | | : | | | | |
Db      403 QRGRSCDVTSNTCLGPSIQTRACSLSKCDTRIRQDGGWSHWPWSSCSVTCGVGNITRIR 462

Qy      268 SCTNPAPLNGGAFCEGQNVQKTAC-ATLCPVDGSWSPWSKWSACGLDCT---HWRSRECS 323
        | : | | || |: | : | | ||: || || | || | : | | : |
Db      463 LCNSPVPQMGGKNCKGSGRETKACQGAPCPIDGRWSPWSPWSACTVTCAGGIRERTRVCN 522

Qy      324 DPAPRNGGEECQGTDLDRNCTSDLCVHSASGPEDVALYVGLIAVAVCLVLLLLVLILVY 383
        | |: ||: | | : : | | | | | | | | | | |
Db      523 SPEPQYGGKACVGDVQERQMCNKRSC-----PVDGCLSNPCFPGAQC----- 564

Qy      384 CRKKEGLDSDVDASSILTSGFQPVSI--KPSKADNPHLLTIQPDLSSTTTT-----TYQ 434
        | | | : || | | : :: : ||: : | : |
Db      565 -----SSFPDGS-WSCGFPCVGFGLNGTHCEDLDECALVPDICEFSTSKVPRCVNTQP 615

Qy      435 GSLC----PRQDGPSP 446
        | | | | | | |
Db      616 GFHCLPCPPRYRGNQP 631

```

RESULT 8

US-08-808-982-8

; Sequence 8, Application US/08808982

; Patent No. 5939271

; GENERAL INFORMATION:

```

;   APPLICANT: Tessier-Lavigne, Marc
;   APPLICANT: Leonardo, E. David
;   APPLICANT: Hink, Lindsay
;   APPLICANT: Masu, Masayuki
;   APPLICANT: Kazuko, Keino-Masu

```

```

; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-808-982-8

```

```

Query Match          6.1%; Score 294; DB 2; Length 102;
Best Local Similarity 56.4%; Pred. No. 3.9e-20;
Matches 57; Conservative 16; Mismatches 28; Indels 0; Gaps 0;

```

```

Qy      608 EEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVAAAKRLKLLLFAPVACTSLEYNIR 667
      || : | || | || : : || : || : | : | || : | || | || | : |
Db      2 EETLNTPCYXQLEPRACXILLDQLGTYVFTGESYSRSAVKRLQLAVFAPALCTSLEYSLR 61

Qy      668 VYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNL 708
      || | | || | || | : || : || | | : || : | | | | | | |
Db      62 VYCLEDPVALKEVLELERTLGGYLV EEPKPLMFKDSYHNL 102

```

RESULT 9

US-09-306-902A-8

```

; Sequence 8, Application US/09306902A
; Patent No. 6277585
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
;           Leonardo, E. David
;           Hink, Lindsay
;           Masu, Masayuki
;           Kazuko, Keino-Masu

```



```

; TITLE OF INVENTION: Inhibiting Angiogenesis
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
; STREET: 100 South Wacker Drive, Suite 960
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-4002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/01652
; FILING DATE: 19930222
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/841,656
; FILING DATE: 24-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/464,369
; FILING DATE: 12-JAN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Fentress, Susan B.
; REGISTRATION NUMBER: 31,327
; REFERENCE/DOCKET NUMBER: 92005-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)-456-8000
; TELEFAX: (312)-456-7776
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US93-01652-1

```

```

Query Match          5.6%; Score 268.5; DB 5; Length 239;
Best Local Similarity 33.5%; Pred. No. 4.4e-17;
Matches 52; Conservative 23; Mismatches 61; Indels 19; Gaps 4;

```

```

Qy      207 VVRQARLADTANYTCVAKNIVAR-----RRSASAAVIVYVNGGWSWTWTEWSVCSASC 258
      : :: | |: | | :: | :| :||| |: || || :|
Db      88 IQQRGRSCDSLNNRCEGSSVQTRTCHIQECDKRFKQ-----DGGWSHWSWPSSCSVTC 140

Qy      259 GRGWQKRSRCTNPAPLNGGAFCEGQNVQKTAC-ATLCPVDGSWSPWSKWSACGLDC--- 314
      | | | | | :|:| | |||: : || ||:| | ||| | | : |
Db      141 GDGVITRIRLCNSPSPQMNLGPCEGEARETKACKKDACPINGGWGPWSPWDICSVTCGGG 200

Qy      315 THWRSRECSDPAPRNGGEECQGTDLDTNRNCTSDLC 349
      ||| |:|:|:|: || :| | : : | |
Db      201 VQKRSLCNPAPQFGGLDCVGDVTENQICNKQDC 235

```

RESULT 11
 US-08-313-288B-20
 ; Sequence 20, Application US/08313288B
 ; Patent No. 5750502
 ; GENERAL INFORMATION:
 ; APPLICANT: Jessell, Thomas M. and AviHu Klar
 ; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
 ; TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/313,288B
 ; FILING DATE: January 5, 1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 278-0400
 ; TELEFAX: (212) 391-0526
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1170 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-313-288B-20

Query Match 5.6%; Score 268.5; DB 1; Length 1170;
 Best Local Similarity 32.9%; Pred. No. 6.3e-16;
 Matches 51; Conservative 24; Mismatches 61; Indels 19; Gaps 4;

Qy 207 VVRQARLADTANYTCVAKNIVAR-----RRSASAAVIVYVNGGWSTWTEWSVCSASC 258
 : :: | |: | | :: | :| :||| |: || || :|
 Db 399 IQQRGRSCDSLNNRCEGSSVQTRTCHIQECDKRFKQ-----DGGWSHWSPWSSCSVTC 451
 Qy 259 GRGWQKRSRSC TNPAPLNGGAFCEGQNVQKTAC-ATLCPVDGSWSPWSKWSACGLDC--- 314
 | | | | | :|:| | |||: : || ||:| | || | | : |
 Db 452 GDGVITRIRLCNSPSPQMNGKPCGEARETKACKKDACPINGGWGPWSPWDICSVTCGGG 511
 Qy 315 THWRSRECS DPAPRNGGEECQGTDL DTRNCTSDLC 349
 ||| |:| |: ||:| | : : | |
 Db 512 VQKRSRLC NNPTPQFGGKDCVGDVTENQICNKQDC 546

RESULT 12
 US-08-985-526-3
 ; Sequence 3, Application US/08985526
 ; Patent No. 6080728
 ; GENERAL INFORMATION:
 ; APPLICANT: Mixson, James A
 ; TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
 ; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN
 GENE
 ; TITLE OF INVENTION: THERAPY
 ; NUMBER OF SEQUENCES: 43
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Connolly, Bove, Lodge, & Hutz
 ; STREET: 1220 Market Street, P.O. Box 2207
 ; CITY: Wilmington
 ; STATE: Delaware
 ; COUNTRY: U.S.A.
 ; ZIP: 19899
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/985,526
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/608,845
 ; FILING DATE: 16-JUL-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McMorro Jr., Robert G
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (302) 658-9141
 ; TELEFAX: (302) 658-5613
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 441 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 US-08-985-526-3

Query Match 5.2%; Score 249.5; DB 3; Length 441;
 Best Local Similarity 26.2%; Pred. No. 7.9e-15;
 Matches 88; Conservative 35; Mismatches 112; Indels 101; Gaps 16;

Qy 75 FKCNGEW-----VRQVDHVIERSTDGSSGLPTM-----EVRINVSQQ----V 113
 || :| | | | | | | :| | | | | : : :
 Db 132 FKQDGGWSHWSPWSSCSVTCDGVITRITLCNSPSPQMNGKPCEGEARETKACKKDACPI 191
 Qy 114 EKVFGLLEEYWCQCVAWSSSGTTSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPP 173
 :| | | | | : : | | :| | : |||
 Db 192 NGGWGPWSPWDICSVTCGGGVQKRSRLCV---DSRMTEENKELANELR-----RPP 239
 Qy 174 ----EGIPPAEVEWLRNED-LVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVA 228

```

      |      |:: ||: ||  :      | :| |
Db      240 LCYHNG-----VQYRNNEEWTVDSCTE-----CHCQNSVT 269
Qy      229 RRRSASAAVIVYVNG-----GWSTWTEWSVCSASCGRGWQKRSRSC 269
      : | :| : |      ||| |:|: || ||| | |:| |||
Db      270 ICKKVSCPIMPCSNATVPDGECCPRCWPSDSADDGWSPWSEWTSCSTSCGNGIQQRGRSC 329
Qy      270 TNPAPLNGGAFCEGQNVQKTAC-ATLC----PVDGSWSPWSKWSACGLDC---THWRSRE 321
      : || || :|| | | | || || || |:| : | |
Db      330 DS---LNNR--CEGSSVQTRTCHIQECDKRFKQDGGWSHWSPWSSCSVTCDGQVITRITL 384
Qy      322 CSDPAPRNGGEECQGTDLDRNCTSDLC-VHSASGP 356
      |: |:|: |: |:| :|: | | | :: ||
Db      385 CNSPSPQMNGKPCGEARETKACKKDACPINGGWGP 420

```

RESULT 13

US-08-313-288B-15

; Sequence 15, Application US/08313288B

; Patent No. 5750502

; GENERAL INFORMATION:

; APPLICANT: Jessell, Thomas M. and AviHu Klar

; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A

; TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/313,288B

; FILING DATE: January 5, 1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 40028-A-PCT-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 278-0400

; TELEFAX: (212) 391-0526

; TELEX:

; INFORMATION FOR SEQ ID NO: 15:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 469 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO
US-08-313-288B-15

Query Match 5.1%; Score 243; DB 1; Length 469;
Best Local Similarity 39.5%; Pred. No. 3.6e-14;
Matches 45; Conservative 14; Mismatches 43; Indels 12; Gaps 4;

Qy 243 GGWSTWTEWSVCSASCGRGWQKRSRSCNTPAPLNGGAFCEGQNVQKTACAT--LCPVDGS 300
| | | | | | | | : | : | : | : | | | | : | | | : | | | :
Db 137 GGWSGWGPWEPCSVTC SKGTRTRRRACNHPAPKCGG-HCPGQAQSEACDTQQVCPTHGA 195

Qy 301 WSPWSKWSACGLDC-----THWRSRECS DPAP--RNGGEECQGTDL DTRNCT 345
| : | | : | | | | | | | | : | : | | | : | | |
Db 196 WATWGPWTPCSASCHGGPHEPKETR SRKCSA PEPSQKPPGKPCPGLAYEQRRCT 249

RESULT 14

US-08-985-526-1

; Sequence 1, Application US/08985526
; Patent No. 6080728
; GENERAL INFORMATION:
; APPLICANT: Mixson, James A
; TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN
GENE
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street, P.O. Box 2207
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19899
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,526
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,845
; FILING DATE: 16-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: McMorrow Jr., Robert G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 658-9141
; TELEFAX: (302) 658-5613
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-985-526-1

Query Match 5.0%; Score 238; DB 3; Length 218;
Best Local Similarity 39.3%; Pred. No. 3e-14;
Matches 48; Conservative 16; Mismatches 44; Indels 14; Gaps 6;

```
Qy      244 GWSTWTEWSVCSASCGRGWQKRSRSCSTNPAPLNGGAFCEGQNVQKTAC-ATLC-----PVD 298
          ||| |:|: || ||| | |:| ||| :  ||  ||| :||  |  |  |
Db      81 GWSPWSEWTSCSTSCGNGIQQRGRSCDS---LNNR--CEGSSVQTRTCHIQCEDKRFKQD 135

Qy      299 GSWSPWSKWSACGLDC---THWRSRECS DPAPRNGGEECQGTDLDTNRCTSDLC-VHSAS 354
          | || || |:| : |  |  |:|: |: |:| : |:| | | ::
Db     136 GGWSHWSPWSSCSVTGCGDVITRITNLCSPSPQMNGKPCEGREAETKACKKDACPINGGW 195

Qy      355 GP 356
          ||
Db     196 GP 197
```

RESULT 15

US-09-540-245A-15
; Sequence 15, Application US/09540245A
; Patent No. 6270984
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,245A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/065,544
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 1395
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-540-245A-15

Query Match 4.9%; Score 234.5; DB 3; Length 1395;
Best Local Similarity 20.7%; Pred. No. 1.5e-12;
Matches 187; Conservative 104; Mismatches 273; Indels 341; Gaps 43;

```
Qy      4 RPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGA-----NPDLLPHFLVEPEDVYIVKN 58
          |  | || | :|| |  :| :|  :| :: |  | |: : ||
Db     28 RMWLLPAWLLLVLVA-----SNGLPAVRGQYQSPRIEH----PTDLVVKKN 70

Qy      59 KPVLLVCK--AVPATQIFFKCNGEWV---RQVDHVIERSTDGSSGLPTMEVRINVSRRQQV 113
          :|  | ||  |  | : :|| |  : | ::  ||  |
Db     71 EPATLNCKVEGKPEPTIEWFKDGEPVSTNEKKSHRVQFKDGALFFYRTM-----QG 121

Qy     114 EKVFGLEEYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPP 173
          :|  |||  ||| :  |  |: | ::|| || :|  ||  |: : :| | ||
```

Db 122 KKEQDGGGEYW--CVAKNRVGQAVSRHASLQIAVLRDDFRVEPKDTRVAKGETALLECGPP 179

Qy 174 EGIPPAEVEWLRN----EDLVDPSL--DPNVYITREHSLVVRQARLADTANYTCVAKNIV 227
:| | : | : : : | | | : | : : | | | : | : |

Db 180 KGIPEPTLIWIKDGVPLDDLKAMSGASSRVIRVDGGNLLISNVEPIDEGNYKCIAQNLV 239

Qy 228 ARRRSASAAVIVYVN-----GGWSTWTEWSVCSASCGRG-----WQK- 264
| | : | : | | | : | : | | | : |

Db 240 GTRESSYAKLIVQVKPYFMKEPKDQVMLYGQTATF-----HCSVGGDPPPKVLWKKE 291

Qy 265 -----RSRSCNPAPLNGGAF-CEGQN--VQKTACATL----- 294
: | : | | : | : | | | : | : |

Db 292 EGNIPVSRARILHDEKSLEISNITPTDEGTYVCEAHNNVGQISARASLIVHAPPNFTKRP 351

Qy 295 -----CPVDGWSWPSKWSACGL-----DCTHWSRECSDPAPRNGGEEC 334
| | : | | : | : : | : | : |

Db 352 SNKKVGLNGVVQLPCMASGNPPPSVFWTKEGVSTLMFPNSSHGRQYVAADGT-----L 404

Qy 335 QGTDLDTRNCTSDLCVHSASGPEDVALYVGLIAVAVCLVLLLLVLILVYCRKKEGLDSDV 394
| | : | | | | | | |

Db 405 QITDV-----RQEDEGY--VCSAF-----SV 424

Qy 395 ADSSILTSGFQPVSIKPSKADN--PHLLTIQPDLTSTTTTTYQGS--CPRQDGPSPKF 448
| | : | : | | : | | | : | : | | : |

Db 425 VDSSTVR-----VFLQVSSVDERPPPIIQIGP--ANQTLPGKSVATLPCRATGNPSPRI 476

Qy 449 Q-LTNGHLLSPLGGGRHTLHHSSPTSEAEFVSRLSTQNYFRSLPRGTSNMTYGTFNFLG 507
: | : | : | : | : | : | : |

Db 477 KWFHDGHAVQ--AGNRYSIQGSRLRVDLQLSDSGTYTCTASGERGETS----- 524

Qy 508 GRLMIPNTGISLLIPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTLLSPIVSCGPPGVL 567
: | : | | | | | | |

Db 525 -----WAATLTVEKPGSTSLHRAA-----DPSTYPAPPGT- 554

Qy 568 LTRPVILAMDHCGEPSDPSWSLR-LKKQSCGS-----WEDVLH-L 606
| : | : | | | | | : | | : |

Db 555 ---PKVLNV-----SRTSISLRWAKSQEKPGAVGPIIGYTVEYFSPDLQGTGWIVAAHRV 605

Qy 607 GEEAPSHLYYCQLEASACYVF-----TEQLGRFALVGEALSVA- 644
| : : : | | | | : | | |

Db 606 GD---TQVTISGLTPGTSYVFLVRAENTQGISVPSGLSNVIKTIEADFDAASANDLSAAR 662

Qy 645 ---AAKRLKLLLFAPVACTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHF 701
| : : : : : : | : | | : | | : |

Db 663 TLLTGKSVELIDASAINASAVRLE---WMLHVSAD-----EKYVEGLRI-----HY 705

Qy 702 KDS-----YHNLRL-----SIHDVPSSLWKSLLVS 727
| : | : : : : | : | : |

Db 706 KDASVPSAQYHSITVMDASAESFVVGNLKKYTKYEFFLTPFFETIEGQPSN---SKTALT 762

Qy 728 YQEIP 732
| : : |

Db 763 YEDVP 767

Search completed: July 6, 2004, 14:36:12
Job time : 24 secs

OM protein - protein search, using sw model

Run on: July 6, 2004, 14:30:11 ; Search time 27 Seconds
(without alignments)
3199.259 Million cell updates/sec

Title: US-10-624-932-2
Perfect score: 4791
Sequence: 1 MAVRPGLWPALLGIVLAWL.....AVAGLGQPDAGLFTVSEAEC 898

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match Length	DB	ID	Description
	Score	Match				
1	977	20.4	919	2	T32541	unc-5 protein - Ca
2	977	20.4	947	1	B44294	unc-5 protein, lon
3	298.5	6.2	1584	2	T00026	brain-specific ang
4	296.5	6.2	1172	1	TSHUP2	thrombospondin 2 p
5	293	6.1	1074	2	JC5928	semaphorin F precu
6	293	6.1	1172	2	A42587	thrombospondin 2 p
7	276	5.8	1444	2	T18856	angiogenesis inhib
8	275	5.7	984	2	T00326	hypothetical prote
9	275	5.7	1522	2	T00028	brain-specific ang
10	274.5	5.7	1572	2	T00027	brain-specific ang
11	270.5	5.6	1170	2	A40558	thrombospondin 1 p
12	268.5	5.6	1170	1	TSHUP1	thrombospondin 1 p
13	263	5.5	1178	1	A39804	thrombospondin pre

14	243	5.1	469	1	S29126	properdin precurs
15	229	4.8	437	2	S05478	properdin - mouse
16	226	4.7	254	2	T15952	hypothetical prote
17	221.5	4.6	1265	1	A37967	neural cell adhesi
18	215	4.5	788	2	T25061	hypothetical prote
19	215	4.5	1651	2	T14160	transmembrane rece
20	208	4.3	1612	2	T30805	dutt1 protein - mo
21	191.5	4.0	1344	2	T14316	rig-1 protein - mo
22	191	4.0	1863	2	S46217	protein-tyrosine-p
23	188.5	3.9	957	2	T15976	hypothetical prote
24	186	3.9	423	2	T29549	hypothetical prote
25	181.5	3.8	1273	2	T42405	sax-3 protein - Ca
26	181	3.8	1736	2	A47747	tight junction pro
27	178	3.7	1745	2	A46431	tight junction-ass
28	175	3.7	1907	2	S50893	protein-tyrosine-p
29	172	3.6	837	2	T00355	hypothetical prote
30	169.5	3.5	934	1	A34372	complement C6 prec
31	168.5	3.5	152	2	D89753	protein F11C7.2 [i
32	168	3.5	860	2	T16892	hypothetical prote
33	162.5	3.4	654	2	T29247	hypothetical prote
34	161	3.4	1501	2	I58148	protein-tyrosine-p
35	159.5	3.3	951	2	T00017	gene ADAMTS-1 prot
36	159	3.3	805	2	T34212	hypothetical prote
37	158.5	3.3	2165	2	T21371	hypothetical prote
38	157	3.3	550	2	T47158	hypothetical prote
39	156.5	3.3	807	2	A38152	F-spondin - rat
40	156	3.3	584	1	C8HUA	complement C8 alph
41	155	3.2	1499	2	I50212	protein-tyrosine-p
42	155	3.2	1898	2	S46216	leukocyte antigen-
43	150.5	3.1	1437	2	T31093	probable protein-t
44	149.5	3.1	712	2	A45638	immunodominant mic
45	148.5	3.1	206	2	A45517	coccidiosis-relate

ALIGNMENTS

RESULT 1

T32541

unc-5 protein - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Jan-2000

C;Accession: T32541

R;Latreille, P.

submitted to the EMBL Data Library, December 1997

A;Description: The sequence of *C. elegans* cosmid B0273.

A;Reference number: Z21187

A;Accession: T32541

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-919 <LAT>

A;Cross-references: EMBL:AF036698; PIDN:AAB88355.1; GSPDB:GN00022; CESP:B0273.4a

A;Experimental source: strain Bristol N2; clone B0273

C;Genetics:

A;Gene: unc-5; CESP:B0273.4a

A;Map position: 4

A;Introns: 41/3; 108/1; 142/3; 201/1; 323/2; 553/1; 858/3

Db 713 LCESNDFILNEKG---NLCICIEDVIPGFSCDGPVEVVEISETQHRFV---AQNGLHCSLK 766
 Qy 750 LERVSPSTSDLACKLWVWQVEGDGQSFSINFNITKDTRFAELLALESEAGVPALVGPSAF 809
 : | : :: |:| : : :: : : : | | | : |
 Db 767 FRPKEINGSQFSTRVIVYQKASSTEPVM--EVSNEPELYDATSEEREKGSVCV----EF 820
 Qy 810 KIPFLIRQKIISLDPCCRRGADWRTLAQKLHLDHLSFFASKP--SPTAMILNLWEARH 867
 ::|| :: :: || | :||| ||:|||| | :| |||| | ||:::|:||||
 Db 821 RLPFGVKDELARLLDMPNESHSDWRGLAKKLHYDRYLQFFASFPDCSPTSLLLDLWEASS 880
 Qy 868 FPNGN-LSQLAAAVAGLGQPD 888
 : : | : :|:||||
 Db 881 SGSARAVPDLQLTRVMGRPDA 902

RESULT 2

B44294

unc-5 protein, long form - *Caenorhabditis elegans*

N;Contains: unc-5 protein, short form

C;Species: *Caenorhabditis elegans*

C;Date: 30-Apr-1993 #sequence_revision 28-Jul-1995 #text_change 05-Nov-1999

C;Accession: B44294; T32540; A44294

R;Leung-Hagesteijn, C.; Spence, A.M.; Stern, B.D.; Zhou, Y.; Su, M.W.;

Hedgecock, E.M.; Culotti, J.G.

Cell 71, 289-299, 1992

A;Title: UNC-5, a transmembrane protein with immunoglobulin and thrombospondin type 1 domains, guides cell and pioneer axon migrations in *C. elegans*.

A;Reference number: A44294; MUID:93046629; PMID:1384987

A;Contents: variety Bergerac

A;Accession: B44294

A;Molecule type: DNA

A;Residues: 1-947 <LEU>

A;Cross-references: GB:S47168; NID:g258527; PIDN:AAB23867.1; PID:g258529

A;Note: sequence extracted from NCBI backbone (NCBIN:116668, NCBIN:116670, NCBIN:116672, NCBIN:116674, NCBIN:116676, NCBIN:116678, NCBIN:116680, NCBIN:116682, NCBIN:116685, NCBIN:116688)

A;Note: authors translated the codon CTA for residue 642 as Val; sequence shown follows the authors' translation

A;Note: mRNA lacking the first exon is equally prevalent

R;Latreille, P.

submitted to the EMBL Data Library, December 1997

A;Description: The sequence of *C. elegans* cosmid B0273.

A;Reference number: Z21187

A;Accession: T32540

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-947 <LAT>

A;Cross-references: EMBL:AF036698; PIDN:AAB88356.1; GSPDB:GN00022; CESP:B0273.4b

A;Experimental source: strain Bristol N2; clone B0273

C;Genetics:

A;Gene: unc-5

A;Map position: 4

A;Introns: 28/1; 69/3; 136/1; 170/3; 229/1; 351/2; 581/1; 886/3

C;Function:

A;Description: required for guidance of pioneering axons and cells migrating dorsally along the body wall; proposed to be a receptor on the surface of the motile cells

C;Superfamily: unc-5 protein; immunoglobulin homology; SH3 homology;
 thrombospondin type 1 repeat homology
 C;Keywords: alternative splicing; duplication; glycoprotein; receptor;
 transmembrane protein
 F;30-947/Product: unc-5 protein, short form #status predicted <ALT>
 F;46-116/Domain: immunoglobulin homology <IM1>
 F;153-211/Domain: immunoglobulin homology <IM2>
 F;229-300/Domain: thrombospondin type 1 repeat homology #status atypical <THR1>
 F;301-354/Domain: thrombospondin type 1 repeat homology <THR2>
 F;365-390/Domain: transmembrane #status predicted <TMM>
 F;512-559/Domain: SH3 homology <SH3>
 F;53-114,65-112,160-209/Disulfide bonds: #status predicted
 F;206/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 20.4%; Score 977; DB 1; Length 947;
 Best Local Similarity 28.7%; Pred. No. 1.2e-62;
 Matches 265; Conservative 168; Mismatches 379; Indels 110; Gaps 31;

Qy	49	EPEDVYIVKNKPVLLVCKAVPATQIFFKCNGEWVRQVDHVIER--STDGSSGLPTMEVRI	106
		: : :: : : : : : : : : : :: :	
Db	37	QPKSGYVIRNKPLRLQCRANHATKIRYKCSSKWID--DSRIEKLIGTDSTSGVGYIDASV	94
Qy	107	NVSRQQVEKVFGLLEEYWCQCVAWSSSG-----TTKSQKAYIRIARLRKNFEQEPLAKEVS	161
		: : : : : : : : : :	
Db	95	DISRIDVDTSGHVDAFQCQCYA---SGDDDQDVVASDVATVHLAYMRKHFLKSPVAQRVQ	151
Qy	162	LEQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPNVPYITREHSLVVRQARLADTANYTC	221
		: : : : : : : : : :	
Db	152	EGTTLQLPCQAPESDPKAELTWYKDGVVVQP--DANVIRASDGLIMSAAARLSDSGNYTC	209
Qy	222	VAKNIVARRRSASAAVIVYVNGGWSTWTEW-SVCSASCG-----RGWQKR	265
		: : : : : :	
Db	210	EATNVANSRKTDPEVQIYVDGGWSESWPWIGTCHVDCPLLRQHAHRI RDPHDVLPHQRR	269
Qy	266	SRSCNTPAPLNGGAFCEGQNVQKTACATLCPVDGSWSPWSKWSACGLDCTHWSRECSDP	325
		: : : : : : : : : :	
Db	270	TRTCNNPAPLNDGEYCKGEEEMTRSCVKPCKLDGGWSSWSDWSACSSSCHRYRTRACTVP	329
Qy	326	APRNGGEECQGTDLDRNCTSDLCVHSASG--PEDVALYVGLIAVAVCLVLLLVLILVY	383
		: : : : : : : : : : :	
Db	330	PPMNGGQPCFGDDLMTQECPAQLCTADSSRIVISDTAVYGSVASIFIVASFILAILAMFC	389
Qy	384	CR-----KKEGLDSDVADSSILTSGFQPVSIKPSKADNPHELLTI-----	422
		: : : : : : : : : : : :	
Db	390	CKRGNSSKSKPLKPQKMNSEKAGGIYYS---EPPGVRLLLEHQHGTLLGEKISSCSQYF	446
Qy	423	-QPDLSTTTT-----TYQGSILCPRQDGPSPKFQLTNGHLLSPLGGGRHTLHHSSPT-SE	474
		: :	
Db	447	EPPPLPHSTTLRSGKSAFSGYSSTRNAGSRAALIQCSSSSSGSGGKRTMLRTSSSNCS	506
Qy	475	AEEFVSRLSTQNYFRSLPRGTS-NMTYGTFNFLGGRLMIPNTGISLLIPPDaiprGKIYE	533
		: : : : : : : : : :	
Db	507	DDNYATLYDYMEDKSVLGLDTSQNIVAAQIDSNARLSLSKSGARLIVPELAVEGEKM--	564
Qy	534	IYLT LHKPEDVRLPLAGCQTLLSPIVSCGPPGV-----LLTRPVILAMDHCGEPS-D	585
		: : : : : : :	
Db	565	LYLAVSDTLTDQPHLKPIESALSPVIVIGQCDVSMASAHNLRP VVVSFRHCASTFPRD	624

Qy 586 SWSLRLKKQSCEGS-WEDVLHLGEEAPSHLYYCQLEASA-----CYVFTEQLGRFAL 636
 :| | : ||| |: : :||| : : | | | :| | | |
 Db 625 NWQFTL--YADEGSGWQKAVTIGEENLNTNMFVQFEQPGKKNDGFGWCHVMTYSLARLML 682
 Qy 637 VGEAL--SVAAAKRLKLLLFAVACTSLE--YNIRVYCLHDTHDALKEVVQLEKQLGGQL 692
 | :||| |: | :| : : :|||: :| |: | : | :|
 Db 683 AGHPRRNSLSAAKRVHLAVFGPTMSAYRRPFELRVYCVPETGAAMESVWKQED--GSRL 740
 Qy 693 IQEPR--VLHFKDSYHNLRLSIHDV-PSSLWKSLLVSYQEIPFYHIWNGTQRYLHCTFT 749
 : | :|: | | : | || | :| | : | |||:
 Db 741 LCESNDFILNEKG---NLCICIEDVIPGFSCDGPVEVVEISETQHRFV---AQNGLHCSLK 794
 Qy 750 LERVSPSTSDLACKLWVWQVEGDGQSFSINFNITKDTFAELLALESEAGVPALVGPSAF 809
 : | : :| |: | : : : : : : | | | : |
 Db 795 FRPKEINGSQFSTRVIVYQKASSTEPMMV--EVSNEPELYDATSEEREKGSVCV----EF 848
 Qy 810 KIPFLIRQKIISSLDPPCRRGADWRTLAQKLHLDSHLSFFASKP--SPTAMILNLWEARH 867
 :|| : : : || | :||| ||:| | :| ||| | ||: :|:| | |
 Db 849 RLPFGVKDELARLLDMPNESHSDWRGLAKKLHYDRYLQFFASFPDCSPTSLLLDLWEASS 908
 Qy 868 FPNGN-LSQLAAAVAGLGQPD 888
 : : | : :|||
 Db 909 SGSARAVPDLLQTLRVMGRPDA 930

RESULT 3

T00026

brain-specific angiogenesis inhibitor 1 - human

N;Alternate names: BAI1 protein

C;Species: Homo sapiens (man)

C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 12-Feb-1999

C;Accession: T00026

R;Nishimori, H.; Shiratsuchi, T.; Urano, T.; Kimura, Y.; Kiyono, K.; Tatsumi, K.; Yoshida, S.; Ono, M.; Kuwano, M.; Nakamura, Y.

submitted to the EMBL Data Library, June 1997

A;Reference number: Z14064

A;Accession: T00026

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-1584 <NIS>

A;Cross-references: EMBL:AB005297; NID:d1175078; PID:d1024528

A;Experimental source: brain

C;Genetics:

A;Gene: GDB:BAI1

A;Cross-references: GDB:9838088; OMIM:602682

A;Map position: 8q24-8q24

C;Superfamily: thrombospondin type 1 repeat homology

F;408-462/Domain: thrombospondin type 1 repeat homology <THR3>

Query Match 6.2%; Score 298.5; DB 2; Length 1584;

Best Local Similarity 33.5%; Pred. No. 4.4e-13;

Matches 78; Conservative 35; Mismatches 91; Indels 29; Gaps 11;

Qy 124 CQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPEGIPPAEVEW 183
 | | :||| : :| : :| | : | | | | | | |
 Db 309 CNREACGPAGRTSSRSQSLRSTDARR---REELGDEL---QQFGFPA-PQTGDPAAE-EW 360

Qy	184	LRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAAVIVYVNG	243
		: : :: : : : : :	
Db	361	--SPWSVCSSSTCGEGWQTR-----TRFCVSSSYSTQCSGPLREQRLCNNSAVCPVHG	410
Qy	244	GWSTWTWEVSVCASACGRGWQKRSRCTNPAPLNGGAFCEGQNQKTAC-ATLCP---VDG	299
		: : : : : :	
Db	411	AWDESWPSLSCSSTCGRGFRDRTRCTR--PPQFGGNPCGEKPEKTKFCNIALCPGRAVDG	468
Qy	300	SWSPWKWSACGLDCT---HWRSDRECDPAPRNNGEECQGTDLDRNCTSDLCL	349
		::: : : : : : :	
Db	469	NWNEWSSWSACSASCQSQRQORTRECNGPS--YGGAECOGHWVETRDCLFOOC	519

F;493-549/Domain: thrombospondin type 1 repeat homology <THR3>
 F;553-588/Domain: EGF homology <EGF1>
 F;652-691/Domain: EGF homology <EGF>
 F;928-930/Region: cell attachment (R-G-D) motif
 F;151,316,330,457,584,710,1069/Binding site: carbohydrate (Asn) (covalent)
 #status predicted
 F;167-226/Disulfide bonds: #status predicted
 F;266,270/Disulfide bonds: interchain #status predicted
 F;612/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 6.2%; Score 296.5; DB 1; Length 1172;
 Best Local Similarity 30.5%; Pred. No. 4.1e-13;
 Matches 78; Conservative 28; Mismatches 105; Indels 45; Gaps 9;

```

Qy      209 RQARLADTANYTCVAKNIVARRRSASAA-VIVYVNGGWSTWTEWSVCSASCGRGWQKRSR 267
          :: | | : ||: :| | | | : :||| |: || || :|| | | |
Db      403 QGRGSCDVTSTCLGPSIQTRACSLSKCDTRIRQDGGWSHWSPWSSCSVTCGVGNITRIR 462

Qy      268 SCTNPAPLNGGAFCEGQNVQKTAC-ATLCPVDGSWSPWSKWSACGLDCT---HWSRECS 323
          | :| | || |:| : || ||:| | ||| ||| : | | :| | :
Db      463 LCNSPVPQMGGKNCKGSGRETKACQGAPCPIDGRWSPWSPWSACTVTTCAGGIRERTRVCN 522

Qy      324 DPAPRNGGEECQGTDLDRNCTSDLCVHSASGPEDVALYVGLIAVAVCLVLLLLVLILVY 383
          | |: ||: | | : : | | | | | | | | | | | |
Db      523 SPEPQYGGKACVGDVQERQMCNKRSC-----PVDGCLSNPCFPGAQC----- 564

Qy      384 CRKKEGLDSDVADSSILTSGFQPVSI--KPSKADNPHLLTIQPDLTSTTTT-----TYQ 434
          | | | : || || : :: : ||: :|: |
Db      565 -----SSFPDGS-WSCGFPCVGFNGTHCEDLDECALVPDICFSTSKVPRCVNTQP 615

Qy      435 GSLC----PRQDGPSP 446
          | | || | |
Db      616 GFHCLPCPPRYRGNQP 631

```

RESULT 5

JC5928

semaphorin F precursor - human

C;Species: Homo sapiens (man)

C;Date: 10-Apr-1998 #sequence_revision 08-May-1998 #text_change 17-Nov-2000

C;Accession: JC5928

R;Simmons, A.D.; Pueschel, A.W.; McPherson, J.D.; Overhauser, J.; Lovett, M.
 Biochem. Biophys. Res. Commun. 242, 685-691, 1998

A;Title: Molecular cloning and mapping of human semaphorin F from the Cri-du-
 chat candidate interval.

A;Reference number: JC5928; MUID:98125554; PMID:9464278

A;Accession: JC5928

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-1074 <SIM>

A;Cross-references: GB:U52840; NID:g2772583; PIDN:AAC09473.1; PID:g2772584

A;Experimental source: brain

C;Comment: This protein disrupts normal brain development and leads to some of
 the features of Cri-du-chat.

C;Genetics:

A;Gene: sema f

C;Superfamily: human semaphorin F; thrombospondin type 1 repeat homology

F;1-20/Domain: signal sequence #status predicted <SIG>
 F;50-533/Domain: semaphorin #status predicted <SEM>
 F;840-896/Domain: thrombospondin type 1 repeat homology <THR3>
 F;971-993/Domain: transmembrane #status predicted <TMM>

Query Match 6.1%; Score 293; DB 2; Length 1074;
 Best Local Similarity 45.8%; Pred. No. 6.6e-13;
 Matches 54; Conservative 11; Mismatches 49; Indels 4; Gaps 2;

```

Qy      241 VNGGWSTWTEWSVCSASCGRGWQKRSRSCNPAPLNGGAFCEGQNVQKTACATL-CPVDG 299
      ||| || || || || | || : | | | | | | | | | | | | | | | |
Db      783 VNGAWSAWTSWSQCSRDCSRGI RNRKRVCNNPEPKYGGMPCLGPSLEYQECNTLPCPVDG 842

Qy      300 SWSPWSKWSACGLDC---THWRSRECSDPAPRNGGEECQGTDLDTNRCTSDLCVHSAS 354
      || || |: | | : |:| ||: || | |: | | : | : | | |
Db      843 VWSCWSPWTKCSATCGGGHYMRTRSCSNPAPAYGGDICLGLHTEEALCNTQPCPESWS 900
  
```

RESULT 6

A42587

thrombospondin 2 precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999

C;Accession: A42587; A39851

R;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
 J. Biol. Chem. 267, 3274-3281, 1992

A;Title: Characterization of mouse thrombospondin 2 sequence and expression
 during cell growth and development.

A;Reference number: A42587; MUID:92147683; PMID:1371115

A;Accession: A42587

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-1172 <LAH>

A;Cross-references: GB:L07803; GB:M87275; NID:g340421; PIDN:AAA53064.1;
 PID:g567241

A;Note: sequence extracted from NCBI backbone (NCBIP:81502)

R;Bornstein, P.; O'Rourke, K.; Wikstrom, K.; Wolf, F.W.; Katz, R.; Li, P.;
 Dixit, V.M.

J. Biol. Chem. 266, 12821-12824, 1991

A;Title: A second, expressed thrombospondin gene (Thbs2) exists in the mouse
 genome.

A;Reference number: A39851; MUID:91302287; PMID:1712771

A;Accession: A39851

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-873 <BOR>

A;Cross-references: GB:M64866; NID:g201994; PIDN:AAA40432.1; PID:g201995

C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat
 homology; von Willebrand factor type C repeat homology

C;Keywords: calcium binding; glycoprotein

F;319-377/Domain: von Willebrand factor type C repeat homology <VWC>

F;380-431/Domain: thrombospondin type 1 repeat homology <THR1>

F;436-492/Domain: thrombospondin type 1 repeat homology <THR2>

F;493-549/Domain: thrombospondin type 1 repeat homology <THR3>

F;553-588/Domain: EGF homology <EGF1>

F;652-691/Domain: EGF homology <EGF>

Query Match 6.1%; Score 293; DB 2; Length 1172;
Best Local Similarity 38.0%; Pred. No. 7.4e-13;
Matches 60; Conservative 22; Mismatches 66; Indels 10; Gaps 5;

```
Qy      209 RQARLADTANYTCVAKNIVARRRS-ASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSR 267
          :: | | : ||: :| | | : |||| | : || || :|| | | |
Db      403 QRGRSCDVTSNTCLGPSIQTRTCSLGGKCDTRIRQNGGWSHWSPWSSCSVTTCGVGNVTRIR 462

Qy      268 SCTNPAPLNGGAFCEGQNVQKTAC-ATLCPVDGWSWSPWSKWSACGLDCT---HWSRECS 323
          | :| | || |:| : | ||:| | |||| |||| : | || | :
Db      463 LCNSPVPQMGGKNCKGSGRETKPCQRDPCPIDGRWSPWSPWSACTVTCAGGIRERSRVCN 522

Qy      324 DPAPRNGGEECQG--TD---LDTRNCTSDLCVHSASGP 356
          | | : ||:| | | : : |:| | | : : |
Db      523 SPEPQYGGKDCVGDVTEHQMCNKRS CPIDGCLSNPCFP 560
```

RESULT 7

T18856

angiogenesis inhibitor homolog - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C;Accession: T18856; T24653

R;McMurray, A.

submitted to the EMBL Data Library, July 1995

A;Reference number: Z19031

A;Accession: T18856

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1444 <WIL>

A;Cross-references: EMBL:Z50004; PIDN:CAA90293.1; GSPDB:GN00028; CESP:C02B4.1

A;Experimental source: clone C02B4

R;McMurray, A.

submitted to the EMBL Data Library, July 1995

A;Reference number: Z19917

A;Accession: T24653

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1444 <WI2>

A;Cross-references: EMBL:Z50006; PIDN:CAA90302.1; GSPDB:GN00028; CESP:C02B4.1

A;Experimental source: clone T07C5

C;Genetics:

A;Gene: CESP:C02B4.1

A;Map position: X

A;Introns: 25/3; 70/3; 96/3; 139/3; 187/1; 234/2; 282/3; 376/2; 422/2; 478/3;
509/3; 566/2; 625/1; 696/2; 786/3; 812/2; 878/3; 971/1; 1007/3; 1067/1; 1099/3;
1180/3; 1273/2; 1305/1; 1363/1; 1388/2

Query Match 5.8%; Score 276; DB 2; Length 1444;
Best Local Similarity 27.2%; Pred. No. 1.7e-11;
Matches 73; Conservative 28; Mismatches 97; Indels 70; Gaps 12;

```
Qy      123 WCQCVAWSSSGTTKSQKAYIRIARLRKNFEQ-----EPLAKEVSLEQGIVLPCRPEGI 176
          | : :||: : : | : | | : ||| :|| |
Db      1134 WSEWSSWSAC-----SCFSLTSTRRRFCQVVDPTVQGFCAGAILAQ---IPCAPGSCS 1183

Qy      177 PPAE-----VEW-----LRNEDLVDPSLDPNVYITREHSLVVRQARLADTAN 218
```

```

      | |      | |      : | |      : |      : | |      :
Db      1184 PSAGGWSLWSEWSSCSKDCGDTGHQIRNRMCSSEP-----IPSNRGAYCSG 1228

Qy      219 YT-----CVAKNIVARRRSASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCNPA 273
      | :      | |      | : :      :      | : | | : | | | : | | : | | |
Db      1229 YSFDQRPCVMDNVCSDEK-----VDGGWTDWTAWSECTDYCRNGHRSRTRFCANPK 1279

Qy      274 PLNGGAFCEGQNVQKTAC--ATLCPV-DGSWSPWSKWSACGLDC---THWRSRECSDPAP 327
      | | | | | : :      |      | : | | | | | : |      | | | | |
Db      1280 PSQGGAQCTGSDFELNPCFDPARCHLRDGGWSTWSDWTPCSASCAGFVQTRDRSCSSPEP 1339

Qy      328 RNGGEECQGTDLDTNRCTSDLCVHSASG 355
      : | | : | |      | |      | | : |
Db      1340 K-GGQSCSGLAHQTSLCDLPACDHESDG 1366

```

RESULT 8

T00326

hypothetical protein KIAA0550 - human

C;Species: Homo sapiens (man)

C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000

C;Accession: T00326

R;Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.

DNA Res. 5, 31-39, 1998

A;Title: Prediction of the coding sequences of unidentified human genes. IX. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.

A;Reference number: Z14086; MUID:98290545; PMID:9628581

A;Accession: T00326

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-984 <NAG>

A;Cross-references: EMBL:AB011122; NID:g3043623; PIDN:BAA25476.1; PID:g3043624

A;Experimental source: brain

C;Genetics:

A;Note: KIAA0550

C;Superfamily: thrombospondin type 1 repeat homology

F;344-398/Domain: thrombospondin type 1 repeat homology <THR3>

Query Match 5.7%; Score 275; DB 2; Length 984;

Best Local Similarity 39.0%; Pred. No. 1.2e-11;

Matches 57; Conservative 20; Mismatches 53; Indels 16; Gaps 6;

```

Qy      220 TCVA-----KNIVARRRSASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCNPA 273
      | | | :      :      | :      : | : | | | : | | | : | | | |
Db      317 TCVSPYGTCHCSGPLRESRVCNNALCPVHGVWEEWSPWSLCSFTCGRGQRTTRTRSC--P 374

Qy      274 PLNGGAFCEGQNVQKTAC--ATLCPVDGSWSPWSKWSACGLDC---THWRSRECSDPAPRN 329
      | | | | | |      | | | | | | | | : |      | | | : | : | :
Db      375 PQYGGRPCGEPETHHKPCNIALCPVDGQWQEWSSWSQCSVTCSNGTQQRSRQCT--AAAH 432

Qy      330 GGEECQGTDLDTNRCTSDLCVHSASG 355
      | | | | : | : | : | : | : | : |
Db      433 GGSECRGPWAESRECYNPEC--TANG 456

```

RESULT 9

T00028

brain-specific angiogenesis inhibitor 3 - human

N;Alternate names: BAI3 protein

C;Species: Homo sapiens (man)

C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000

C;Accession: T00028

R;Shiratsuchi, T.; Nishimori, H.; Ichise, H.; Nakamura, Y.; Tokino, T.

Cytogenet. Cell Genet. 79, 103-108, 1997

A;Title: Cloning and characterization of BAI2 and BAI3, novel genes homologous to brain-specific angiogenesis inhibitor 1 (BAI 1).

A;Reference number: Z14066; MUID:98194217; PMID:9533023

A;Accession: T00028

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-1522 <SHI>

A;Cross-references: EMBL:AB005299; NID:g3021700; PIDN:BAA25363.1; PID:g3021701

A;Experimental source: brain

C;Genetics:

A;Gene: GDB:BAI3

A;Cross-references: GDB:9838090; OMIM:602684

A;Map position: 6q12-6q12

C;Superfamily: thrombospondin type 1 repeat homology

F;344-398/Domain: thrombospondin type 1 repeat homology <THR3>

Query Match 5.7%; Score 275; DB 2; Length 1522;
Best Local Similarity 39.0%; Pred. No. 2.1e-11;
Matches 57; Conservative 20; Mismatches 53; Indels 16; Gaps 6;

Qy 220 TCVA-----KNIVARRRSASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCSTNPA 273
|||: : | : : |:| | |: ||:| | :||| : |:| | |
Db 317 TCVSPYGTHCSGPLRESRVCNNALCPVHGVWEEWSPWSLCSFTCGRGQRTRTRRSCT--P 374

Qy 274 PLNGGAFCEGQNVQKTAC-ATLCPVDGSWSPWSKWSACGLDC---THWRSRECSDPAPRN 329
| || ||| | ||||| | || || | : | | |||:| : | :
Db 375 PQYGGRPCEGPETHHKPCNIALCPVDGQWQEWSSWSQCSVTCSNGTQQRSRQCT--AAAH 432

Qy 330 GGEQCQGTDLDTNRCTSDLCVHSASG 355
|| ||:| :| | : | :| |
Db 433 GGSECRGPWAESRECYNPEC--TANG 456

RESULT 10

T00027

brain-specific angiogenesis inhibitor 2 - human

N;Alternate names: BAI2 protein

C;Species: Homo sapiens (man)

C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000

C;Accession: T00027

R;Shiratsuchi, T.; Nishimori, H.; Ichise, H.; Nakamura, Y.; Tokino, T.

Cytogenet. Cell Genet. 79, 103-108, 1997

A;Title: Cloning and characterization of BAI2 and BAI3, novel genes homologous to brain-specific angiogenesis inhibitor 1 (BAI 1).

A;Reference number: Z14066; MUID:98194217; PMID:9533023

A;Accession: T00027

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-1572 <SHI>
A;Cross-references: EMBL:AB005298; NID:g3021698; PIDN:BAA25362.1; PID:g3021699
A;Experimental source: brain
C;Genetics:
A;Gene: GDB:BAI2
A;Cross-references: GDB:9838089; OMIM:602683
A;Map position: lp35-lp35

Query Match 5.7%; Score 274.5; DB 2; Length 1572;
Best Local Similarity 19.2%; Pred. No. 2.4e-11;
Matches 176; Conservative 108; Mismatches 307; Indels 327; Gaps 38;

Qy	173	PEGIPPAEVEWLRNEDLVDPSPDPNVY-----ITREHSIVVRQARL	213
		: : : : : :	
Db	271	PEEPPKVKTKQWPRAD-----EPGLYMAQTGDPAEEWSPWSVCSLTCGQLQVR-TRS	323
Qy	214	ADTANYTCVAKNIVARRRSASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCNPA	273
		:: : : : : : : : :	
Db	324	CVSSPYGTLCSGPLRETRPCNNSATCPVHGVEEWGWSLCSRSCGRGSRSRMRTCV--P	381
Qy	274	PLNGGAFCEGQNVQKTACA-TLCPVDGSWSPWSKWSACGLDC---THWRSRECSDPAPR-	328
		: : : : :	
Db	382	PQHGGKACEGPELQTKLCSMAACPVEGQWLEWGPWGPCSTSCANGTQQRSRKCSVAGPAW	441
Qy	329	-----NGGEECQ	335
		:	
Db	442	ATCTGALTDTRECSNLECPATDSKWGPWNAWSLCSKTCDTGWQRRFRMCQATGTQGYPC	501
Qy	336	GTDLDTNRCTSDLC--VHSASGPEDVAL-----	361
		: : :	
Db	502	GTGEEVKPCSEKRCPAFHEMCRDEYVMLMTWKAAAGEIIYNKCPPNASGSASRRCLLSA	561
Qy	362	----YVGLIAVAVCL---VLLLLVLILVYCRKKEGLSDVADSSIILTSQFQPVSIKPSKA	414
		: : : : : : : : : : : : :	
Db	562	QGVAYWGLPSFARCISHEYRYLYLSLREHLAKQRMMLAGEGMSQVVRS-LQELLARRTYY	620
Qy	415	DNPHLLTIQPDLSSTTTTTTYQGSCLPRQDGPSPKFQLT-----NGHLLSPLGG	461
		: : : : : : : : : :	
Db	621	SGDLLFSVDILRNVTDTFKRATYVPSADDVQRFFQVVSFMVDAENKEKWDDAQQVSP--G	678
Qy	462	GRHTLHHSSPTSEAEFEV-----SRLSTQNYFRSLPRG-----TSNMTYGTFTN	504
		: : : : : : : :	
Db	679	SVHLLR-----VVEDFIHLVGDAKAFQSSSLIVTDNLVISIQREPVSASVSSDITFPMRG	732
Qy	505	FLG-----GRLMIPNTGISLLIP-----PDAIPRGK-----	530
		: : : :	
Db	733	RRGMKDWRHSEDRLFLPKEVLSLSSPGKPATSGAAGSPGRGRGPGTVPPGPGHSHQRL	792
Qy	531	-----IYE-IYLT LHKPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVIL	574
		: : : : : :	
Db	793	PADPDESSYFVIGAVLYRTLGLILPPP---RPPLAVTSRVMT--VTVRPPTQPPAEPLIT	847
Qy	575	A-----MDHCGEPSPDWSLRLKKQSCEGSWEDVLHLGEEAPSHLYYCQ-LEASACYV--	626
		: : : : : : :	
Db	848	VELSYIINGTTDPHCASWDYS-RADASSGDWD-----TENCQTLETQAAHTRC	894
Qy	627	FTEQLGRFALVGE-----ALSVAALKRLKLLLFAPVACTSLEYNIRVYCLHDTHDALKEV	681

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      : | ||:: : | : : |:: | : | : : |
Db      895 QCQHLSTFAVLAQPPKDLTLELAGSPSVPLVIGCAVSCMALLTLLAIYA-----AFWRF 948

Qy      682 VQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSSLWKSLLVSYQEIPFYHIWNGTQ 741
      :: | : : | || : |:: : || : : |
Db      949 IKSERSI-----ILLNFCLSI--LASNI---LILVGQSRVLSKGVCTMTA 988

Qy      742 RYLHCTFTLERVSPSTSDLACKLWV-----WQVEGDG 773
      : || | | : ||
Db      989 AFLHFFF-----LSSFCWVLTEAWQSYLAVIGRMRTLVRKRFLCLGWGLPALV 1037

Qy      774 QSFSINFNITKDTRFAELLALESEAG-VPALVGPSA-----FKIPFLIRQKI-----IS 821
      : | : | || : | | : | || : | | : : | : ||
Db      1038 VAVSVGFTRTKGYGTSSYCWLSEGLLAFVGPAAVIVLVNMLIGIIVFNKLMARDGIS 1097

Qy      822 SLDPPCRRGAD---WRTL 836
      | |:: | : |
Db      1098 DKSKKQRAGSERCWASL 1115

```

RESULT 11

A40558

thrombospondin 1 precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 20-Aug-1999

C;Accession: A40558; A37905; B42587; S68787

R;Lawler, J.; Duquette, M.; Ferro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.

Genomics 11, 587-600, 1991

A;Title: Characterization of the murine thrombospondin gene.

A;Reference number: A40558; MUID:92128941; PMID:1774063

A;Accession: A40558

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1170 <LAW>

A;Cross-references: GB:M62449; GB:M62450; GB:M62451; GB:M62452; GB:M62453; GB:M62454; GB:M62455; GB:M62456; GB:M62457; GB:M62458; GB:M62459; GB:M62460; GB:M62461; GB:M62462; GB:M62463; GB:M62464; GB:M62465; GB:M62466; GB:M62467; GB:M62468; GB:M62469; GB:M62470; NID:g511867; PIDN:AAA50611.1; PID:g511869

R;Bornstein, P.; Alfi, D.; Devarayalu, S.; Framson, P.; Li, P.

J. Biol. Chem. 265, 16691-16698, 1990

A;Title: Characterization of the mouse thrombospondin gene and evaluation of the role of the first intron in human gene expression.

A;Reference number: A37905; MUID:90375546; PMID:2398070

A;Accession: A37905

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-490 <BOR>

A;Cross-references: GB:J05605; GB:J05606; NID:g201991; PIDN:AAA40431.1; PID:g554390

R;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M. J. Biol. Chem. 267, 3274-3281, 1992

A;Title: Characterization of mouse thrombospondin 2 sequence and expression during cell growth and development.

A;Reference number: A42587; MUID:92147683; PMID:1371115

A;Accession: B42587

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA
 A;Residues: 1-1152,'P',1154-1170 <LAH>
 A;Cross-references: GB:M87276
 A;Note: sequence extracted from NCBI backbone (NCBIP:81501)
 R;Chen, H.; Aeschlimann, D.; Nowlen, J.; Mosher, D.F.
 FEBS Lett. 387, 36-41, 1996
 A;Title: Expression and initial characterization of recombinant mouse
 thrombospondin 1 and thrombospondin 3.
 A;Reference number: S68787; MUID:96234006; PMID:8654563
 A;Accession: S68787
 A;Molecule type: protein
 A;Residues: 19-26,'X',28-37 <CHE>
 C;Complex: homotrimer, disulfide linked
 C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat
 homology; von Willebrand factor type C repeat homology
 C;Keywords: calcium binding; glycoprotein; homotrimer
 F;1-18/Domain: signal sequence #status predicted <SIG>
 F;19-1170/Product: thrombospondin 1 #status predicted <MAT>
 F;317-375/Domain: von Willebrand factor type C repeat homology <VWC>
 F;378-429/Domain: thrombospondin type 1 repeat homology <THR1>
 F;434-490/Domain: thrombospondin type 1 repeat homology <THR2>
 F;491-547/Domain: thrombospondin type 1 repeat homology <THR3>
 F;551-586/Domain: EGF homology <EGF>
 F;248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 5.6%; Score 270.5; DB 2; Length 1170;
 Best Local Similarity 32.2%; Pred. No. 3.2e-11;
 Matches 57; Conservative 24; Mismatches 71; Indels 25; Gaps 5;

Qy	207	VVRQARLADTANYTCVAKNIVAR-----RRSASAAVIVYVNGGWSTWTEWSVCSASC	258
		: :: : :: : : :	
Db	399	IQQRGRSCDSLNNRCEGSSVQTRTCHIQECDKRFKQ-----DGGWSHWSPWSSCSVTC	451
Qy	259	GRGWQKRSRCTNPAPLNGGAFCEGQNVQKTAC-ATLCPVDGWSWPSKWSACGLDC---	314
		: : : : :	
Db	452	GDGVITRIRLCNSPSPQMNGKPCGEARETKACKKDACPINGGWGPWSPWDICSVTCGGG	511
Qy	315	THWRSRECSDPAPRNGGEECQGTDLDRNCTSDLCVHSASGPEDVALYVGLIAVAVC	371
		: : : : : :	
Db	512	VQRRSRLCNNPTPQFGGKDCVGDVTENQVCNKQDC-----PIDGCLSNPCFAGAKC	562

RESULT 12

TSHUP1
 thrombospondin 1 precursor - human
 C;Species: Homo sapiens (man)
 C;Date: 23-Aug-1987 #sequence_revision 03-Aug-1995 #text_change 17-Nov-2000
 C;Accession: A26155; A34274; A30140; A25812; A05172; A42927
 R;Lawler, J.; Hynes, R.O.
 J. Cell Biol. 103, 1635-1648, 1986
 A;Title: The structure of human thrombospondin, an adhesive glycoprotein with
 multiple calcium-binding sites and homologies with several different proteins.
 A;Reference number: A26155; MUID:87057617; PMID:2430973
 A;Accession: A26155
 A;Molecule type: mRNA
 A;Residues: 1-1170 <LAW>
 A;Cross-references: GB:X04665; NID:g37137; PIDN:CAA28370.1; PID:g37138

A;Note: parts of this sequence, including the amino end of the mature protein, were determined by protein sequencing
 R;Laherty, C.D.; Gierman, T.M.; Dixit, V.M.
 J. Biol. Chem. 264, 11222-11227, 1989
 A;Title: Characterization of the promoter region of the human thrombospondin gene. DNA sequences within the first intron increase transcription.
 A;Reference number: A34274; MUID:89291870; PMID:2544587
 A;Accession: A34274
 A;Molecule type: DNA
 A;Residues: 1-166 <LAH>
 A;Cross-references: GB:J04835
 R;Hennessy, S.W.; Frazier, B.A.; Kim, D.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotwein, P.; Frazier, W.A.
 J. Cell Biol. 108, 729-736, 1989
 A;Title: Complete thrombospondin mRNA sequence includes potential regulatory sites in the 3' untranslated region.
 A;Reference number: A30140; MUID:89139590; PMID:2918029
 A;Accession: A30140
 A;Molecule type: mRNA
 A;Residues: 1-83,'A',85-522,'A',524-1170 <HEN>
 A;Cross-references: EMBL:X14787; NID:g37464; PIDN:CAA32889.1; PID:g37465
 A;Note: parts of this sequence, including the amino end of the mature protein, were determined by protein sequencing
 R;Kobayashi, S.; Eden-McCutchan, F.; Framson, P.; Bornstein, P.
 Biochemistry 25, 8418-8425, 1986
 A;Title: Partial amino acid sequence of human thrombospondin as determined by analysis of cDNA clones: homology to malarial circumsporozoite proteins.
 A;Reference number: A25812; MUID:87157592; PMID:3030396
 A;Accession: A25812
 A;Molecule type: mRNA
 A;Residues: 1-83,'A',85-397 <KOB>
 A;Cross-references: GB:M25631; NID:g538353; PIDN:AAA36741.1; PID:g538354
 R;Dixit, V.M.; Hennessy, S.W.; Grant, G.A.; Rotwein, P.; Frazier, W.A.
 Proc. Natl. Acad. Sci. U.S.A. 83, 5449-5453, 1986
 A;Reference number: A05172; MUID:86287276; PMID:3461443
 A;Accession: A05172
 A;Molecule type: mRNA
 A;Residues: 1-83,'A',85-374,'RC' <DIX>
 A;Cross-references: GB:M14326; NID:g340005; PIDN:AAA61237.1; PID:g553801
 A;Note: parts of this sequence, including the amino end of the mature protein, were determined by protein sequencing
 R;Sun, X.; Skorstengaard, K.; Mosher, D.F.
 J. Cell Biol. 118, 693-701, 1992
 A;Title: Disulfides modulate RGD-inhibitable cell adhesive activity of thrombospondin.
 A;Reference number: A42927; MUID:92348511; PMID:1379247
 A;Accession: A42927
 A;Molecule type: protein
 A;Residues: 987-1003 <SUN>
 A;Note: Cys-992 is shown to have a free sulfhydryl
 C;Genetics:
 A;Gene: GDB:THBS1; TSP1; TSP
 A;Cross-references: GDB:120438; OMIM:188060
 A;Map position: 15q15-15q15
 A;Introns: 23/1
 A;Note: the list of introns may be incomplete
 C;Complex: homotrimer, disulfide linked

C;Function:
A;Description: participates in cell migration and adhesion, and in platelet aggregation
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; von Willebrand factor type C repeat homology
C;Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-1170/Product: thrombospondin 1 #status predicted <MAT>
F;317-375/Domain: von Willebrand factor type C repeat homology <VWC>
F;378-429/Domain: thrombospondin type 1 repeat homology <THR1>
F;434-490/Domain: thrombospondin type 1 repeat homology <THR2>
F;491-547/Domain: thrombospondin type 1 repeat homology <THR3>
F;551-586/Domain: EGF homology <EGF1>
F;650-689/Domain: EGF homology <EGF2>
F;926-928/Region: cell attachment (R-G-D) motif
F;171-232/Disulfide bonds: #status predicted
F;248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;270,274/Disulfide bonds: interchain #status predicted
F;610/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F;1051/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 5.6%; Score 268.5; DB 1; Length 1170;
Best Local Similarity 32.9%; Pred. No. 4.4e-11;
Matches 51; Conservative 24; Mismatches 61; Indels 19; Gaps 4;

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Qy      207 VVRQARLADTANYTCVAKNIVAR-----RRSASAAVIVYVNGGWSTWTEWSVCSASC 258
          : :: | | : | | : : | : | : ||| | : || || : |
Db      399 IQQRGRSCDSLNNRCEGSSVQTRTCHIQECDKRFKQ-----DGGWSHWSPWSSCSVTC 451

Qy      259 GRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTAC-ATLCPVDGSWSPWSKWSACGLDC--- 314
          | | | | | : | | | | : : | | | : | | | | | : |
Db      452 GDGVITRIRLCNSPSPQMNGKPCGEARETKACKKDACPINGGWGPWSPWDICSVTCGGG 511

Qy      315 THWRSRECSDPAPRNGGEECQGTDLDTNRCTSDLC 349
          ||| | : | | : | : | | : : | |
Db      512 VQKRSRLCNNPTPQFGGKDCVGDVTENQICNKQDC 546

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RESULT 13

A39804

thrombospondin precursor - chicken

C;Species: Gallus gallus (chicken)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C;Accession: A39804

R;Lawler, J.; Duquette, M.; Ferro, P.

J. Biol. Chem. 266, 8039-8043, 1991

A;Title: Cloning and sequencing of chicken thrombospondin.

A;Reference number: A39804; MUID:91217026; PMID:2022631

A;Accession: A39804

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1178 <LAW>

A;Cross-references: GB:M60853; NID:g212763; PIDN:AAA51437.1; PID:g212764

C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; von Willebrand factor type C repeat homology

F;325-383/Domain: von Willebrand factor type C repeat homology <VWC>

F;386-437/Domain: thrombospondin type 1 repeat homology <THR1>
 F;442-498/Domain: thrombospondin type 1 repeat homology <THR2>
 F;499-555/Domain: thrombospondin type 1 repeat homology <THR3>
 F;658-697/Domain: EGF homology <EGF>

Query Match 5.5%; Score 263; DB 1; Length 1178;
 Best Local Similarity 36.2%; Pred. No. 1.1e-10;
 Matches 58; Conservative 16; Mismatches 70; Indels 16; Gaps 5;

Qy 210 QARLADTANYTCVAKNIVARRRS-ASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRS 268
 : | | | : | | : : ||| | : || | : || | |
 Db 410 RGRSCDVTRSACTGPHIQTRMCSFKKCDHRIRQDGGWSHWSPSSCSVTCGVGNITRIRL 469

Qy 269 CTNPAPLNGGAFCEGQNVQKTACATL-CPVDGWSWSPWSKWSACGLDC---THWRSRECS 324
 | : | | || | | : | ||| : | || | || | : | || | :
 Db 470 CNSPIPQMGGKNCVGNGRETEKCEKAPCPVNGQWGPWSPWSACTVTCTGGGIRERSRLCNS 529

Qy 325 PAPRNGGEECQGTDLDT-----RNCTSDLCVHSASGP 356
 | | : || : | | || | : | | : : |
 Db 530 PEPQYGGKPCVG---DTKQHDMCNKRDCPIDGCLSNPCFP 566

RESULT 14

S29126

properdin precursor [validated] - human

N;Alternate names: factor P

C;Species: Homo sapiens (man)

C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 17-Nov-2000

C;Accession: S29126; S16150; A05319; T45112; T45113

R;Nolan, K.F.; Kaluz, S.; Higgins, J.M.G.; Goundis, D.; Reid, K.B.M.

Biochem. J. 287, 291-297, 1992

A;Title: Characterization of the human properdin gene.

A;Reference number: S29126; MUID:93038568; PMID:1417780

A;Accession: S29126

A;Molecule type: DNA

A;Residues: 1-469 <NOL1>

A;Cross-references: EMBL:X70872; NID:g35679; PIDN:CAA50220.1; PID:g35680

R;Nolan, K.F.; Schwaebler, W.; Kaluz, S.; Dierich, M.P.; Reid, K.B.M.

Eur. J. Immunol. 21, 771-776, 1991

A;Title: Molecular cloning of the cDNA coding for properdin, a positive regulator of the alternative pathway of human complement.

A;Reference number: S16150; MUID:91184288; PMID:2009915

A;Accession: S16150

A;Molecule type: mRNA

A;Residues: 1-456, 'R', 458-469 <NOL2>

A;Cross-references: EMBL:X57748

R;Reid, K.B.M.; Gagnon, J.

Mol. Immunol. 18, 949-959, 1981

A;Reference number: A05319; MUID:82195224; PMID:7341961

A;Accession: A05319

A;Molecule type: protein

A;Residues: 28-53, 'Q', 55-59, 'G', 61, 'I', 63; 137-138, 'P', 140-141, 'P', 143-144, 'X', 146-148, 'Y', 150, 'S', 152, 'Y', 154-156, 'XSXGXA'; 162-163, 'E', 165-172, 'X', 174-176, 'X', 178, 'V', 180; 223-228, 'X', 230-232, 'GX', 235-238, 'GH', 241-245; 248-251, 'X', 253-257, 'P', 259, 'G', 261, 'XPP', 265-266, 'X', 268-269; 280-285, 'X', 287-290, 'X', 292, 'H', 294-300, 'SXXX', 305-307, 'X', 309-315, 'K', 317; 333-

341,343-357,'X',359-362,'EXE';393-404,'QK',407;421-427,'R',429-443,'TKV',447-448,'XX',451,'RX',454-455 <REI>
R;Westberg, J.; Nordin-Fredrikson, G.; Truedsson, L.; Sjöholm, A.G.; Uhlen, M.
submitted to the EMBL Data Library, May 1997
A;Reference number: Z22914
A;Accession: T45112
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-54,'X',56-73,'X',75-99,'W',101-469 <WES1>
A;Cross-references: EMBL:AF005665; PIDN:AAB63280.1
A;Experimental source: genomic DNA from individual with properdin deficiency
type II
A;Accession: T45113
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-60,'X',62-413,'D',415-452,'XX',455-469 <WE2>
A;Cross-references: EMBL:AF005666; PIDN:AAC51626.1
A;Experimental source: genomic DNA from individual with properdin deficiency
type III
R;Hartmann, S.; Hofsteenge, J.
J. Biol. Chem. 275, 28569-28574, 2000
A;Title: Properdin, the positive regulator of complement, is highly C-
mannosylated.
A;Reference number: A59360; MUID:20435812; PMID:10878002
A;Contents: annotation
A;Note: identification and location of C-mannosylation sites by mass-
spectroscopy
C;Genetics:
A;Gene: GDB:PFC
A;Cross-references: GDB:120275; OMIM:312060
A;Map position: Xp11.3-Xp11.23
A;Introns: 26/1; 76/2; 135/1; 192/1; 256/1; 314/1; 378/1; 415/2
C;Complex: a mixture of homodimers, homotrimers and homotetramers
C;Function:
A;Description: protects C3 convertase (C3bBb) from rapid inactivation
A;Pathway: complement alternate pathway
C;Superfamily: human properdin precursor; thrombospondin type 1 repeat homology
C;Keywords: complement alternate pathway; glycoprotein; homodimer; homotetramer;
homotrimer; plasma
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-469/Product: properdin #status experimental <MAT>
F;76-128/Domain: thrombospondin type 1 repeat homology <THR1>
F;135-191/Domain: thrombospondin type 1 repeat homology <THR2>
F;192-255/Domain: thrombospondin type 1 repeat homology <THR3>
F;256-313/Domain: thrombospondin type 1 repeat homology <THR4>
F;314-377/Domain: thrombospondin type 1 repeat homology <THR5>
F;378-440/Domain: thrombospondin type 1 repeat homology <THR6>
F;83,86,139,142,145,196,199,260,263,321,324,382,385,388/Modified site: 2'-
mannosyl-tryptophan (Trp) #status experimental
F;428/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 5.1%; Score 243; DB 1; Length 469;
Best Local Similarity 39.5%; Pred. No. 9.2e-10;
Matches 45; Conservative 14; Mismatches 43; Indels 12; Gaps 4;

Qy 243 GGWSTWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACAT--LCPVDGS 300
|||| | | || :| :| :| |:| :|| | | || : || | :|| |:

Db 137 GGWSGWGPWEPCSVTCSKGTTRRRACNHPAPKCGG-HCPGQAQSEACDTQQVCPTHGA 195

Qy 301 WSPWSKWSACGLDC-----THWRSRECSDPAP--RNGGEECQGTDLDTNRNCT 345
 |: | |: | | ||:| | | : |: | | : | ||

Db 196 WATGWPWTPCSASCHGGPHEPKETRSRKCSAPEPSQKPPGKPCPGLAYEQRRCT 249

RESULT 15

S05478

properdin - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 17-Nov-2000

C;Accession: S05478

R;Goundis, D.; Reid, K.B.M.

Nature 335, 82-85, 1988

A;Title: Properdin, the terminal complement components, thrombospondin and the circumsporozoite protein of malaria parasites contain similar sequence motifs.

A;Reference number: S05478; MUID:88318954; PMID:3045564

A;Accession: S05478

A;Molecule type: mRNA

A;Residues: 1-437 <GOU>

A;Cross-references: EMBL:X12905; NID:g53786; PIDN:CAA31389.1; PID:g53787

C;Complex: a mixture of homodimers, homotrimers and homotetramers

C;Function:

A;Description: protects C3 convertase (C3bBb) from rapid inactivation

A;Pathway: complement alternate pathway

C;Superfamily: human properdin precursor; thrombospondin type 1 repeat homology

C;Keywords: complement alternate pathway; glycoprotein; homodimer; homotetramer; homotrimer; plasma

F;45-97/Domain: thrombospondin type 1 repeat homology <THR1>

F;104-160/Domain: thrombospondin type 1 repeat homology <THR2>

F;161-224/Domain: thrombospondin type 1 repeat homology <THR3>

F;225-282/Domain: thrombospondin type 1 repeat homology <THR4>

F;283-345/Domain: thrombospondin type 1 repeat homology <THR5>

F;346-408/Domain: thrombospondin type 1 repeat homology <THR6>

F;52,55,108,111,114,165,168,229,232,290,293,350,353,356/Modified site: 2'-mannosyl-tryptophan (Trp) #status predicted

F;366,396/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 4.8%; Score 229; DB 2; Length 437;

Best Local Similarity 40.4%; Pred. No. 8.7e-09;

Matches 46; Conservative 10; Mismatches 46; Indels 12; Gaps 4;

Qy 243 GGWSTWTEWSVCSASCGRGWQKRSRSCNTPAPLNGGAFCEGQNVQKTACAT--LCPVDGS 300
 |||| | | || :| :| | | | |||| || | |: | || | || |:

Db 106 GGWSEWGPWGPCSVTCSKGTQIRQVCDNPAPKCGG-HCPGEAQQSQACDTQKTCPTHGA 164

Qy 301 WSPWSKWSACGLDC-----THWRSRECSDPAPRN--GGEECQGTDLDTNRNCT 345
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Db 165 WASWGPWSPRSGSCLGGAQEPKETRSRSCSAPAPSHQPPGKPCSGPAYEHKACS 218

Search completed: July 6, 2004, 14:35:37

Job time : 29 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 6, 2004, 14:33:31 ; Search time 56 Seconds
(without alignments)
4991.658 Million cell updates/sec

Title: US-10-624-932-2
Perfect score: 4791
Sequence: 1 MAVRPGLWPALLGIVLAAWL.....AVAGLGQPDAGLFTVSEAE 898

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 1276540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score Match Length DB ID	Description

1	4791	100.0	898	12	US-09-918-779-2	Sequence 2, Appli
2	4791	100.0	898	16	US-10-624-932-2	Sequence 2, Appli
3	4698.5	98.1	899	11	US-09-970-944-2	Sequence 2, Appli
4	4638	96.8	898	10	US-09-933-261-5	Sequence 5, Appli
5	4638	96.8	898	11	US-09-970-944-13	Sequence 13, Appl
6	4638	96.8	898	14	US-10-256-702-5	Sequence 5, Appli
7	4638	96.8	898	14	US-10-240-154-16	Sequence 16, Appl
8	4413	92.1	842	16	US-10-311-623-1	Sequence 1, Appli
9	2845	59.4	544	11	US-09-970-944-14	Sequence 14, Appl
10	2815.5	58.8	557	10	US-09-933-261-6	Sequence 6, Appli
11	2815.5	58.8	557	14	US-10-256-702-6	Sequence 6, Appli
12	2787	58.2	931	11	US-09-970-944-15	Sequence 15, Appl
13	2787	58.2	931	12	US-10-087-684-35	Sequence 35, Appl
14	2787	58.2	931	12	US-09-972-211-121	Sequence 121, App
15	2787	58.2	931	12	US-10-037-417-117	Sequence 117, App
16	2787	58.2	931	12	US-10-096-625-121	Sequence 121, App
17	2787	58.2	1010	12	US-10-218-779-35	Sequence 35, Appl
18	2762	57.6	931	11	US-09-970-944-16	Sequence 16, Appl
19	2762	57.6	931	12	US-09-972-211-125	Sequence 125, App
20	2762	57.6	931	12	US-10-096-625-125	Sequence 125, App
21	2759	57.6	931	12	US-10-037-417-120	Sequence 120, App
22	2755	57.5	931	11	US-09-970-944-17	Sequence 17, Appl
23	2755	57.5	931	12	US-10-087-684-36	Sequence 36, Appl
24	2755	57.5	931	12	US-10-218-779-36	Sequence 36, Appl
25	2755	57.5	931	12	US-09-972-211-122	Sequence 122, App
26	2755	57.5	931	12	US-10-037-417-118	Sequence 118, App
27	2755	57.5	931	12	US-10-037-417-119	Sequence 119, App
28	2755	57.5	931	12	US-10-096-625-122	Sequence 122, App
29	2578.5	53.8	945	12	US-10-087-684-34	Sequence 34, Appl
30	2578.5	53.8	945	12	US-10-218-779-34	Sequence 34, Appl
31	2578.5	53.8	945	12	US-09-972-211-124	Sequence 124, App
32	2578.5	53.8	945	12	US-10-037-417-121	Sequence 121, App
33	2578.5	53.8	945	12	US-10-096-625-124	Sequence 124, App
34	2572.5	53.7	945	12	US-10-087-684-33	Sequence 33, Appl
35	2572.5	53.7	945	12	US-10-218-779-33	Sequence 33, Appl
36	2572.5	53.7	945	12	US-09-972-211-123	Sequence 123, App
37	2572.5	53.7	945	12	US-10-096-625-123	Sequence 123, App
38	2571.5	53.7	943	10	US-09-933-261-7	Sequence 7, Appli
39	2571.5	53.7	943	14	US-10-256-702-7	Sequence 7, Appli
40	2563.5	53.5	933	12	US-10-087-684-2	Sequence 2, Appli
41	2563.5	53.5	933	12	US-10-087-684-4	Sequence 4, Appli
42	2563.5	53.5	933	12	US-10-218-779-2	Sequence 2, Appli
43	2563.5	53.5	933	12	US-10-218-779-4	Sequence 4, Appli
44	2558.5	53.4	945	12	US-10-147-493-146	Sequence 146, App
45	2558.5	53.4	945	12	US-10-145-127-146	Sequence 146, App

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ALIGNMENTS

RESULT 1
 US-09-918-779-2
 ; Sequence 2, Application US/09918779
 ; Publication No. US20030064369A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Taupier, Raymond

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; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/09/918,779
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,762
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,770
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; PRIOR APPLICATION NUMBER: 60/225,470
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,697
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/263,662
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/281,645
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-779-2

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Query Match          100.0%;  Score 4791;  DB 12;  Length 898;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 898;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy	1	MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP	60
Db	1	MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP	60
Qy	61	VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQQVEKVFGL	120
Db	61	VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQQVEKVFGL	120
Qy	121	EYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPPEGIPPAE	180
Db	121	EYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPPEGIPPAE	180
Qy	181	VEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAIVIVY	240
Db	181	VEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAIVIVY	240
Qy	241	VNGGWSTWTEWSVCSASCGRGWQKRSRSCNPNAPLNGGAFCEGQNVQKTACATLCPVDGS	300
Db	241	VNGGWSTWTEWSVCSASCGRGWQKRSRSCNPNAPLNGGAFCEGQNVQKTACATLCPVDGS	300
Qy	301	WSPWSKWSACGLDCTHWRSSRECSDPAPRNGGEECQGTDLDRNCTSDLCVHSASGPEDVA	360
Db	301	WSPWSKWSACGLDCTHWRSSRECSDPAPRNGGEECQGTDLDRNCTSDLCVHSASGPEDVA	360
Qy	361	LYVGLIAVAVCLVLLLLVLILVYCRKKEGLSDSDVADSSILTSGFQPVSIKPSKADNPHLL	420
Db	361	LYVGLIAVAVCLVLLLLVLILVYCRKKEGLSDSDVADSSILTSGFQPVSIKPSKADNPHLL	420
Qy	421	TIQPDISTTTTTTYQGSCLCPRQDGPSPKFQLTNGHLLSPLGGGRHTLHSSPTSEAEFVS	480
Db	421	TIQPDISTTTTTTYQGSCLCPRQDGPSPKFQLTNGHLLSPLGGGRHTLHSSPTSEAEFVS	480
Qy	481	RLSTQNYFRSLPRGTSNMTYGTNFNLGGRLMIPNTGISLLIPDAIPRGKIYEIYLT LHK	540
Db	481	RLSTQNYFRSLPRGTSNMTYGTNFNLGGRLMIPNTGISLLIPDAIPRGKIYEIYLT LHK	540
Qy	541	PEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDWSLRLKKQSCGWS	600
Db	541	PEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDWSLRLKKQSCGWS	600
Qy	601	EDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVA AAKRLKLLFAPVACT	660
Db	601	EDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVA AAKRLKLLFAPVACT	660
Qy	661	SLEYNIRVYCLHDT HDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDPSSLW	720
Db	661	SLEYNIRVYCLHDT HDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDPSSLW	720
Qy	721	KSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSD LACKLWVWQVEGDGQSFSINF	780
Db	721	KSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSD LACKLWVWQVEGDGQSFSINF	780
Qy	781	NITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISSLDPPCRRGADWRTLAQKL	840
Db	781	NITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISSLDPPCRRGADWRTLAQKL	840

; LENGTH: 898
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-624-932-2

Query Match 100.0%; Score 4791; DB 16; Length 898;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 898; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP	60
Db	1	MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP	60
Qy	61	VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQVEKVFGL	120
Db	61	VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQVEKVFGL	120
Qy	121	EYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPGEGIPPAE	180
Db	121	EYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPGEGIPPAE	180
Qy	181	VEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAIVY	240
Db	181	VEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAIVY	240
Qy	241	VNGGWSTWTEWSVCSASCGRGWQKRSRSCNTPAPLNGGAFCEGQNVQKTACATLCPVDGS	300
Db	241	VNGGWSTWTEWSVCSASCGRGWQKRSRSCNTPAPLNGGAFCEGQNVQKTACATLCPVDGS	300
Qy	301	WSPWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDRNCTSDLCVHSASGPEDVA	360
Db	301	WSPWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDRNCTSDLCVHSASGPEDVA	360
Qy	361	LYVGLIAVAVCLVLLLVLILVYCRKKEGLDSDVADSSILTSFGFQPVSIKPSKADNPHLL	420
Db	361	LYVGLIAVAVCLVLLLVLILVYCRKKEGLDSDVADSSILTSFGFQPVSIKPSKADNPHLL	420
Qy	421	TIQPDLSSTTTTYQGSCLPRQDGPSPKFQLTNGHLLSPLGGGRHTLHSSPTSEAEFVS	480
Db	421	TIQPDLSSTTTTYQGSCLPRQDGPSPKFQLTNGHLLSPLGGGRHTLHSSPTSEAEFVS	480
Qy	481	RLSTQNYFRSLPRGTSNMTYGTNFGGRLMIPNTGISLLIPDAIPRGKIYEIYLT LHK	540
Db	481	RLSTQNYFRSLPRGTSNMTYGTNFGGRLMIPNTGISLLIPDAIPRGKIYEIYLT LHK	540
Qy	541	PEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDWSLRLKKQSCEGSW	600
Db	541	PEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDWSLRLKKQSCEGSW	600
Qy	601	EDVLHLGEEAPSHLYYCQEASACYVFTEQLGRFALVGEALSVA AAKRLKLLLFAPVACT	660
Db	601	EDVLHLGEEAPSHLYYCQEASACYVFTEQLGRFALVGEALSVA AAKRLKLLLFAPVACT	660
Qy	661	SLEYNIRVYCLHDT HDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLR LSIHDPSSSLW	720
Db	661	SLEYNIRVYCLHDT HDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLR LSIHDPSSSLW	720

Qy 721 KSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINF 780
 |||
 Db 721 KSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINF 780

Qy 781 NITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISLDPCCRRGADWRTLQKL 840
 |||
 Db 781 NITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISLDPCCRRGADWRTLQKL 840

Qy 841 HLDSHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAVAGLGQPDAGLFTVSEAE 898
 |||
 Db 841 HLDSHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAVAGLGQPDAGLFTVSEAE 898

RESULT 3

US-09-970-944-2

; Sequence 2, Application US/09970944

; Publication No. US20030204052A1

; GENERAL INFORMATION:

; APPLICANT: Herrman, John L

; APPLICANT: Rastelli, Luca

; APPLICANT: Shimkets, Richard A

; TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids Encoding Same and

; TITLE OF INVENTION: Antibodies Directed Against these Proteins

; FILE REFERENCE: 21402-138

; CURRENT APPLICATION NUMBER: US/09/970,944

; CURRENT FILING DATE: 2002-05-02

; PRIOR APPLICATION NUMBER: 60/237,862

; PRIOR FILING DATE: 2000-10-04

; NUMBER OF SEQ ID NOS: 62

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 899

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-970-944-2

Query Match 98.1%; Score 4698.5; DB 11; Length 899;

Best Local Similarity 98.7%; Pred. No. 0;

Matches 888; Conservative 2; Mismatches 7; Indels 3; Gaps 3;

Qy 1 MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP 60
 |||
 Db 1 MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP 60

Qy 61 VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQVEKVFGL 120
 |||
 Db 61 VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGEPTMEVRINVSRRQVEKVFGL 120

Qy 121 EYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPGEGIPPAE 180
 |||
 Db 121 EYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPGEGIPPAE 180

Qy 181 VEWLNRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAIVY 240
 |||
 Db 181 VEWLNRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAIVY 240

Qy	241	VNGGWSTWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNV-QKTACATLCPVDG	299
Db	241	VNGGWSTWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVHVRTVSSLLVSVDG	300
Qy	300	SWSPWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDTNRCTSDLCVHSASGPEDV	359
Db	301	SWSPWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDTNRCTSDLCVHSASGPEDV	360
Qy	360	ALYVGLIAVAVCLVLLLLVLILVYCRKKEGLSDSDVADSSILTSQFQVPSIKPSKADNPHL	419
Db	361	ALYVGLIAVAVCLVLLLLVLILVYCRKKEGLSDSDVADSSILTSQFQVPSIKPSKADNPHL	420
Qy	420	LTIQPDLSSTTTTTYQGSCLPRQDGPSPKFQLTNGHLLSPLGGGRHTLHHSPTSEAEFV	479
Db	421	LTIQPDLS-TTTTTYQGSCLPRQDGPSPKFQLTNGHLLSPLGGGRHTLHHSPTSEAEFV	479
Qy	480	SRLSTQNYFRSLPRGTSNMTYGTFFNLGGRMLIPNTGISLLIPDAIPRGKIYEIYTLH	539
Db	480	SRLSTQNYFRSLPRGTSNMTYGTFFNLGGRMLIPNTGISLLIPDAIPRGKIYEIYTLH	539
Qy	540	KPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDWSLRLKKQSCGS	599
Db	540	KPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDWSLRLKKQSCGS	599
Qy	600	WE-DVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVAAPKRLKLLFAPVA	658
Db	600	WEQDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVAAPKRLKLLFAPVA	659
Qy	659	CTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDPSS	718
Db	660	CTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDPSS	719
Qy	719	LWKSLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSI	778
Db	720	LWKSLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSI	779
Qy	779	NFNITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISLDPCCRRGADWRTLAQ	838
Db	780	NFNITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISLDPCCRRGADWRTLAQ	839
Qy	839	KLHLDHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAVAGLGQPDAGLFTVSEAE	898
Db	840	KLHLDHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAVAGLGQPDAGLFTVSEAE	899

RESULT 4

US-09-933-261-5

; Sequence 5, Application US/09933261

; Publication No. US20030040046A1

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; Leonardo, E. David

; Hink, Lindsay

; Masu, Masayuki

; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 8

```

;      CORRESPONDENCE ADDRESS:
;      ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;      STREET: 268 BUSH STREET, SUITE 3200
;      CITY: SAN FRANCISCO
;      STATE: CALIFORNIA
;      COUNTRY: USA
;      ZIP: 94104
;
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.30
;
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/933,261
;      FILING DATE: 20-Aug-2001
;      CLASSIFICATION: <Unknown>
;
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 08/808,982
;      FILING DATE: <Unknown>
;
;      ATTORNEY/AGENT INFORMATION:
;      NAME: OSMAN, RICHARD A
;      REGISTRATION NUMBER: 36,627
;      REFERENCE/DOCKET NUMBER: UC96-217
;
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (415) 343-4341
;      TELEFAX: (415) 343-4342
;
;      INFORMATION FOR SEQ ID NO: 5:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 898 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: No. US20030040046A1 Relevant
;      TOPOLOGY: No. US20030040046A1 Relevant
;
;      MOLECULE TYPE: peptide
;      SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-933-261-5

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Query Match          96.8%;  Score 4638;  DB 10;  Length 898;
Best Local Similarity 96.0%;  Pred. No. 0;
Matches 862;  Conservative 17;  Mismatches 19;  Indels 0;  Gaps 0;

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Qy      1 MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP 60
        |||
Db      1 MAVRPGLWPVLLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP 60

Qy     61 VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQVEKVFGL 120
        |||
Db     61 VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDSSSGLPTMEVRINVSRRQVEKVFGL 120

Qy    121 EYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPGEGIPPAE 180
        |||
Db    121 EYWCQCVAWSSSGTTKSQKAYIRIAYLRKNFEQEPLAKEVSLEQGIVLPCRPPGEGIPPAE 180

Qy    181 VEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAAVIVY 240
        |||
Db    181 VEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSTSAAVIVY 240

Qy    241 VNGGWSTWTEWSVCSASCGRGWQKRSRSCCTNPAPLNGGAFCEGQNVQKTACATLCPVDGS 300

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Db	241	VNGGWSTWTEWSVCSASCGRGWQKRSRSCNTPAPLNGGAFCEGQNVQKTACATLCPVDGS	300
Qy	301	WSPWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDTNRCTSDLCVHSASGPEDVA	360
Db	301	WSSWSKWSACGLDCTHWSRECSDPAPRNGGEECRGADLDTRNCTSDLCCLHTASCPEDVA	360
Qy	361	LYVGLIAVAVCLVLLLLVLILVYCRKKEGLDSDVADSSILTSQFQPVSIKPSKADNPHLL	420
Db	361	LYIGLVAVAVCLFLLLLALGLIYCRKKEGLDSDVADSSILTSQFQPVSIKPSKADNPHLL	420
Qy	421	TIQPDLSSTTTTTYQGSLSRQDGPSPKFQLTNGHLLSPLGGGRHTLHHSSPTSEAEFVS	480
Db	421	TIQPDLSSTTTTTYQGSLSRQDGPSPKFQLSNGHLLSPLGSGRHTLHHSSPTSEAEFVS	480
Qy	481	RLSTQNYFRSLPRGTSNMTYGTFFNLGGRLMIPNTGISLLIPPDAIPRGKIYEIYTLHK	540
Db	481	RLSTQNYFRSLPRGTSNMTYGTFFNLGGRLMIPNTGISLLIPPDAIPRGKIYEIYTLHK	540
Qy	541	PEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDSSWLRLLKQSCGWS	600
Db	541	PEDVRLPLAGCQTLLSPVSCGPPGVLLTRPVILAMDHCGEPSPDSSWLRLLKQSCGWS	600
Qy	601	EDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVAALKRLKLLFAPVACT	660
Db	601	EDVLHLGEESPSHLYYCQLEAGACYVFTEQLGRFALVGEALSVAATKRLRLLFAPVACT	660
Qy	661	SLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSSLW	720
Db	661	SLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSSLW	720
Qy	721	KSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINF	780
Db	721	KSKLLVSYQEIPFYHIWNGTQQYLHCTFTLERINASTSDLACKVWVWQVEGDGQSFNINF	780
Qy	781	NITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISLDPCCRRGADWRTLAQKL	840
Db	781	NITKDTRFAELLALESEGGVPALVGPSAFKIPFLIRQKIISLDPCCSRGADWRTLAQKL	840
Qy	841	HLDSHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAVAGLGQPDAGLFTVSEAE	898
Db	841	HLDSHLSFFASKPSPTAMILNLWEARHFPNGNLGQLAAVAGLGQPDAGLFTVSEAE	898

RESULT 5

US-09-970-944-13

; Sequence 13, Application US/09970944

; Publication No. US20030204052A1

; GENERAL INFORMATION:

; APPLICANT: Herrman, John L

; APPLICANT: Rastelli, Luca

; APPLICANT: Shimkets, Richard A

; TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids Encoding Same and

; TITLE OF INVENTION: Antibodies Directed Against these Proteins

; FILE REFERENCE: 21402-138

; CURRENT APPLICATION NUMBER: US/09/970,944

```
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 60/237,862
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-970-944-13
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Db 601 EDVLHLGEEPSHLYYCQLEAGACYVFTEQLGRFALVGEALSVAATKRLRLLLFAPVACT 660
 Qy 661 SLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSLIHDVPSSLW 720
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 661 SLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSLIHDVPSSLW 720
 Qy 721 KSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINF 780
 ||||||||||||||||||||:|||||||||:| |||||||:|||||||||:|||
 Db 721 KSKLLVSYQEIPFYHIWNGTQQYLHCTFTLERINASTSDLACKVWVWQVEGDGQSFNINF 780
 Qy 781 NITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISSLDPPCRRGADWRTLAQKL 840
 |||||||||||||||| |||||||||||||||||||:||||| |||||||||
 Db 781 NITKDTRFAELLALESEGGVPALVGPSAFKIPFLIRQKIIASLDPPCSRGA DWRTLAQKL 840
 Qy 841 HLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAE C 898
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 841 HLD SHLSFFASKPSPTAMILNLWEARHFPNGNLGQLAAAVAGLGQPDAGLFTVSEAE C 898

RESULT 6

US-10-256-702-5

; Sequence 5, Application US/10256702

; Publication No. US20030059859A1

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; Leonardo, E. David

; Hink, Lindsay

; Masu, Masayuki

; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/256,702

; FILING DATE: 27-Sep-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/933,261

; FILING DATE: 20-Aug-2001

; APPLICATION NUMBER: 08/808,982

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: OSMAN, RICHARD A

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: UC96-217

; TELECOMMUNICATION INFORMATION:


```

;           TELEPHONE: (415) 343-4341
;           TELEFAX: (415) 343-4342
;   INFORMATION FOR SEQ ID NO: 5:
;           SEQUENCE CHARACTERISTICS:
;               LENGTH: 898 amino acids
;               TYPE: amino acid
;               STRANDEDNESS: No. US20030059859A1 Relevant
;               TOPOLOGY: No. US20030059859A1 Relevant
;           MOLECULE TYPE: peptide
;           SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-256-702-5

```

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Query Match          96.8%;  Score 4638;  DB 14;  Length 898;
Best Local Similarity 96.0%;  Pred. No. 0;
Matches 862;  Conservative 17;  Mismatches 19;  Indels 0;  Gaps 0;

```

```

Qy      1 MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP 60
        |||
Db      1 MAVRPGLWPVLLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP 60

Qy      61 VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRQQVEKVFGL 120
        |||
Db      61 VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDSSSGLPTMEVRINVSRQQVEKVFGL 120

Qy      121 EYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPGIPP 180
        |||
Db      121 EYWCQCVAWSSSGTTKSQKAYIRIAYLRKNFEQEPLAKEVSLEQGIVLPCRPPGIPP 180

Qy      181 VEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASA 240
        |||
Db      181 VEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSTSA 240

Qy      241 VNGGWSTWTEWSVCSASCGRGWQKRSRSCNPNAPLNGGAFCEGQNVQKTACATLCPVD 300
        |||
Db      241 VNGGWSTWTEWSVCSASCGRGWQKRSRSCNPNAPLNGGAFCEGQNVQKTACATLCPVD 300

Qy      301 WSPWSKWSACGLDCTHWSRECS DPAPRNGGEECQGTDLDTNRCTSDLCVHSASGPED 360
        || |||
Db      301 WSSWSKWSACGLDCTHWSRECS DPAPRNGGEECRGADLDTNRCTSDLCCLHTASCPED 360

Qy      361 LYVGLIAVAVCLVLLLLVLILVYCRKKEGLSDVADSSILTS GFQPVSIKPSKADNP 420
        ||: |||
Db      361 LYIGLVAVAVCLFLLLLALGLIYCRKKEGLSDVADSSILTS GFQPVSIKPSKADNP 420

Qy      421 TIQPDLS TTTT TYQGS LCP RQDGPS PKFQLTNGHLLSPLGGGRHTLHHSSPTSEAE 480
        |||
Db      421 TIQPDLS TTTT TYQGS LCSRQDGPS PKFQLSNGHLLSPLGSGRHTLHHSSPTSEAE 480

Qy      481 RLSTQNYFRSLPRGTSNMTYGT FNFLGGRLMIPNTGISLLIPDAIPRGKIYEIYLT 540
        |||
Db      481 RLSTQNYFRSLPRGTSNMAYGT FNFLGGRLMIPNTGISLLIPDAIPRGKIYEIYLT 540

Qy      541 PEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPD SWSLRLKKQSC 600
        |||
Db      541 PEDVRLPLAGCQTLLSPVVS CGPPGVLLTRPVILAMDHCGEPSPD SWSLRLKKQSC 600

Qy      601 EDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVA AAKRLKLLLFAP 660

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      |||:||||| |||:|||||
Db      601 EDVLHLGEESPSHLYYCQLEAGACYVFTEQLGRFALVGEALSVAATKRLRLLLFAPVACT 660
Qy      661 SLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSSLW 720
      |||:|||||
Db      661 SLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSSLW 720
Qy      721 KSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINF 780
      |||:|||||: |||:|||||: |||
Db      721 KSKLLVSYQEIPFYHIWNGTQQYLHCTFTLERINASTSDLACKVWVWQVEGDGQSFNINF 780
Qy      781 NITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISSLDPPCRRGADWRTLQKL 840
      |||:|||||
Db      781 NITKDTRFAELLALESEGGVPALVGPSAFKIPFLIRQKIIASLDPPCSRGAADWRTLQKL 840
Qy      841 HLDSHLSFFASKPSPTAMILNLWEARHFPGNLSQLAAAVAGLGQPDAGLFTVSEAEC 898
      |||:|||||
Db      841 HLDSHLSFFASKPSPTAMILNLWEARHFPGNLSQLAAAVAGLGQPDAGLFTVSEAEC 898

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RESULT 7

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US-10-240-154-16
; Sequence 16, Application US/10240154
; Publication No. US20030175741A1
; GENERAL INFORMATION:
; APPLICANT: Cochran et al.
; TITLE OF INVENTION: SCHIZOPHRENIA RELATED GENES
; FILE REFERENCE: CKFW-P01-006
; CURRENT APPLICATION NUMBER: US/10/240,154
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: PCT/GB01/01486
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-240-154-16

```

```

Query Match          96.8%; Score 4638; DB 14; Length 898;
Best Local Similarity 96.0%; Pred. No. 0;
Matches 862; Conservative 17; Mismatches 19; Indels 0; Gaps 0;

```

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Qy      1 MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP 60
      |||:|||||
Db      1 MAVRPGLWPVLLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP 60
Qy      61 VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQVEKVFGL 120
      |||:|||||
Db      61 VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDSSGLPTMEVRINVSRRQVEKVFGL 120
Qy      121 EYWCQCVAWSSSGTTSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPGIPPAE 180
      |||:|||||
Db      121 EYWCQCVAWSSSGTTSQKAYIRIAYLRKNFEQEPLAKEVSLEQGIVLPCRPPGIPPAE 180
Qy      181 VEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAIVIVY 240

```

Db	181	VEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSTSAAVIVY	240
Qy	241	VNGGWSTWTEWSVCSASCGRGWQKRSRSCNTPAPLNGGAFCEGQNVQKTACATLCPVDGS	300
Db	241	VNGGWSTWTEWSVCSASCGRGWQKRSRSCNTPAPLNGGAFCEGQNVQKTACATLCPVDGS	300
Qy	301	WSPWSKWSACGLDCTHWSRECSDFAPRNGGEECQGTDLDTNRCTSDLCVHSASGPEDVA	360
Db	301	WSSWSKWSACGLDCTHWSRECSDFAPRNGGEECRGADLDTNRCTSDLCCLHTASCPEDVA	360
Qy	361	LYVGLIAVAVCLVLLLLVLILVYCRKKEGLDSDVADSSILTSQFQPVSIKPSKADNPHLL	420
Db	361	LYIGLVAVAVCLFLLLLALGLIYCRKKEGLDSDVADSSILTSQFQPVSIKPSKADNPHLL	420
Qy	421	TIQPDLSSTTTTYQGSICPRQDGPSPKFQLTNGHLLSPLGGGRHTLHHSSPTSEAEFVS	480
Db	421	TIQPDLSSTTTTYQGSICSRQDGPSPKFQLSNGHLLSPLGSGRHTLHHSSPTSEAEFVS	480
Qy	481	RLSTQNYFRSLPRGTSNMTYGTFFNLGGRLMIPNTGISLLIPPDAIPRGKIYEIYTLHK	540
Db	481	RLSTQNYFRSLPRGTSNMAYGTFFNLGGRLMIPNTGISLLIPPDAIPRGKIYEIYTLHK	540
Qy	541	PEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDWSLRLKKQSCEGSW	600
Db	541	PEDVRLPLAGCQTLLSPVSCGPPGVLLTRPVILAMDHCGEPSPDWSLRLKKQSCEGSW	600
Qy	601	EDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVAARKRLKLLFAPVACT	660
Db	601	EDVLHLGEEAPSHLYYCQLEAGACYVFTEQLGRFALVGEALSVAATKRLRLLFAPVACT	660
Qy	661	SLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDPSSLW	720
Db	661	SLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDPSSLW	720
Qy	721	KSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINF	780
Db	721	KSKLLVSYQEIPFYHIWNGTQQYLHCTFTLERINASTDLACKVWVWQVEGDGQSFNINF	780
Qy	781	NITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISSLDPPCRRGADWRTLAQKL	840
Db	781	NITKDTRFAELLALESEGGVPALVGPSAFKIPFLIRQKIIASLDPPCSRAGADWRTLAQKL	840
Qy	841	HLDSHLSFFASKPSPTAMIILNLWEARHFPNGNLSQLAAVAGLGQPDAGLFTVSEAEAC	898
Db	841	HLDSHLSFFASKPSPTAMIILNLWEARHFPNGNLGQLAAVAGLGQPDAGLFTVSEAEAC	898

RESULT 8

US-10-311-623-1

; Sequence 1, Application US/10311623

; Publication No. US20040023244A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.; GRIFFIN, Jennifer A.

; APPLICANT: KALLICK, Deborah A.; TRIBOULEY, Catherine M.

; APPLICANT: YUE, Henry; NGUYEN, Dannel B.

; APPLICANT: TANG, Y. Tom; LAL, Preeti G.

```

; APPLICANT: POLICKY, Jennifer L.; AZIMZAI, Yalda
; APPLICANT: LU, Dyung Aina M.; GRAUL, Richard C.
; APPLICANT: YAO, Monique G.; BURFORD, Neil
; APPLICANT: HAFALIA, April J. A.; BAUGHN, Mariah R.
; APPLICANT: BANDMAN, Olga; ARVIZU, Chandra S.
; APPLICANT: YANG, Junming; XU, Yuming
; APPLICANT: GANDHI, Ameena R.; WARREN, Bridget A.
; APPLICANT: DING, Li; SANJANWALA, Madhusudan M.
; APPLICANT: DUGGAN, Brendan M.; LU, Yan
; TITLE OF INVENTION: RECEPTORS
; FILE REFERENCE: PF-0793 USN
; CURRENT APPLICATION NUMBER: US/10/311,623
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 01/19942
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/214,027
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/228,045
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/255,104
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 842
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040023244A1 6052371CD1
US-10-311-623-1

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Query Match          92.1%; Score 4413; DB 16; Length 842;
Best Local Similarity 93.5%; Pred. No. 0;
Matches 840; Conservative 1; Mismatches 1; Indels 56; Gaps 1;

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Qy      1 MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP 60
      |||
Db      1 MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP 60

Qy     61 VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQQVEKVFGL 120
      |||
Db     61 VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQQVEKVFGL 120

Qy    121 EYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPGEGIPPAE 180
      |||
Db    121 EYWCQCVAWSSSGTTKSQKAYIRIAYLRKNFEQEPLAKEVSLEQGIVLPCRPPGEGIPPAE 180

Qy    181 VEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAIVIVY 240
      |||
Db    181 VEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAIVIVY 240

Qy    241 VNGGWSTWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACATLCPVDGS 300
      |||
Db    241 -----VDGS 244

Qy    301 WSPWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDTNRCTSDLCVHSASGPEDVA 360

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Db	245	:	WSPWSKWSACGLDCTHWSRECS DPAPRNGGEECQGTDLDTNRCTSDLCVHTASGPEDVA	304
Qy	361		LYVGLIAVAVCLVLLLLVLILVYCRKKEGLSDSDVADSSILTS GFQPVSIKPSKADNPHLL	420
Db	305		LYVGLIAVAVCLVLLLLVLILVYCRKKEGLSDSDVADSSILTS GFQPVSIKPSKADNPHLL	364
Qy	421		TIQPDLS TTTT TYQGS LCP RQD GSP K FQ L TNGHLLS PLGGGRHTLHHSSPTSEAEFVS	480
Db	365		TIQPDLS TTTT TYQGS LCP RQD GSP K FQ L TNGHLLS PLGGGRHTLHHSSPTSEAEFVS	424
Qy	481		RLSTQNYFRSLPRGTSNMTYGT FNFLGGRLMIPNTGISLLIPPD AIPRGKIYEIYLT LHK	540
Db	425		RLSTQNYFRSLPRGTSNMTYGT FNFLGGRLMIPNTGISLLIPPD AIPRGKIYEIYLT LHK	484
Qy	541		PEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPS PDSWSLRLKKQSCEGSW	600
Db	485		PEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPS PDSWSLRLKKQSCEGSW	544
Qy	601		EDVLHLGEEAPSHLYYCQLEASAC YVFTEQLGRFALVGEALSVA AAKRLKLLLFAPVACT	660
Db	545		EDVLHLGEEAPSHLYYCQLEASAC YVFTEQLGRFALVGEALSVA AAKRLKLLLFAPVACT	604
Qy	661		SLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSSLW	720
Db	605		SLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSSLW	664
Qy	721		KSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSD LACKLWVWQVEGDGQSFSINF	780
Db	665		KSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSD LACKLWVWQVEGDGQSFSINF	724
Qy	781		NITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISSLDPPCRRGADWRTLAQKL	840
Db	725		NITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISSLDPPCRRGADWRTLAQKL	784
Qy	841		HLDSHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAE	898
Db	785		HLDSHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAE	842

RESULT 9

US-09-970-944-14

; Sequence 14, Application US/09970944

; Publication No. US20030204052A1

; GENERAL INFORMATION:

; APPLICANT: Herrman, John L

; APPLICANT: Rastelli, Luca

; APPLICANT: Shimkets, Richard A

; TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids Encoding Same and

; TITLE OF INVENTION: Antibodies Directed Against these Proteins

; FILE REFERENCE: 21402-138

; CURRENT APPLICATION NUMBER: US/09/970,944

; CURRENT FILING DATE: 2002-05-02

; PRIOR APPLICATION NUMBER: 60/237,862

; PRIOR FILING DATE: 2000-10-04

; NUMBER OF SEQ ID NOS: 62

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-970-944-14

Query Match 59.4%; Score 2845; DB 11; Length 544;
Best Local Similarity 100.0%; Pred. No. 1.5e-236;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	358	DVALYVGLIAVAVCLVLLLLVLILVYCRKKEGLDSDVADSSILTSGFQPVSIKPSKADNP	417
Db	4	DVALYVGLIAVAVCLVLLLLVLILVYCRKKEGLDSDVADSSILTSGFQPVSIKPSKADNP	63
Qy	418	HLLTIQPDLSSTTTTYQGS LCP RQDGPS PKFQLTNGHLLSPLGGGRHTLHHSSPTSEAE	477
Db	64	HLLTIQPDLSSTTTTYQGS LCP RQDGPS PKFQLTNGHLLSPLGGGRHTLHHSSPTSEAE	123
Qy	478	FVSRLSTQNYFRSLPRGTSNMTYGT FNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLT	537
Db	124	FVSRLSTQNYFRSLPRGTSNMTYGT FNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLT	183
Qy	538	LHKPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDWSLRLKKQSCE	597
Db	184	LHKPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDWSLRLKKQSCE	243
Qy	598	GSWEDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVA AAKRLKLLFAPV	657
Db	244	GSWEDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVA AAKRLKLLFAPV	303
Qy	658	ACTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPS	717
Db	304	ACTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPS	363
Qy	718	SLWKS KLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFS	777
Db	364	SLWKS KLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFS	423
Qy	778	INFNITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISSLDPPCRRGADWRTLA	837
Db	424	INFNITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISSLDPPCRRGADWRTLA	483
Qy	838	QKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAE	897
Db	484	QKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAE	543
Qy	898	C 898	
Db	544	C 544	

RESULT 10
US-09-933-261-6
; Sequence 6, Application US/09933261
; Publication No. US20030040046A1
; GENERAL INFORMATION:

Db 121 RHTLHHSSPTSEAEFFVSRLSTQNYFRSLPRGTSNMTYGTFFNLGGRLMIPNTGISLLIP 180
 Qy 523 PDAIPRGKIYEIYLTLLHKPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCSEP 582
 |||||||
 Db 181 PDAIPRGKIYEIYLTLLHKPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCSEP 240
 Qy 583 SPDSWSLRLKKQSCEGSWEDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALS 642
 |||||||
 Db 241 SPDSWSLALKKQSCEGSWEDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALS 300
 Qy 643 VAAAKRLKLLLFAPVACTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFK 702
 |||||||
 Db 301 VAAAKRLKLLLFAPVACTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHLX 360
 Qy 703 DSYHNLRLSIHDPSSLWKSLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLAC 762
 |||||
 Db 361 DSYHNLXLSXHDVPSSLWKSLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLAC 420
 Qy 763 KLWVWQVEGDGQSFSINFNITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIIS 822
 |||||||
 Db 421 KLWVWQVEGDGQSFSINFNITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIIS 480
 Qy 823 LDPPCRRGADWRTLAQKLHLDLHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAG 882
 |||||||
 Db 481 LDPPCRRGADWRTLAQKLHLDLHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAG 540
 Qy 883 LGQPDAGLFT-VSEAE 898
 | : |||||
 Db 541 TXPAGRWLLSQCEAE 557

RESULT 11

US-10-256-702-6

; Sequence 6, Application US/10256702

; Publication No. US20030059859A1

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; Leonardo, E. David

; Hink, Lindsay

; Masu, Masayuki

; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/256,702


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Db      421 KLWVWQVEGDGQSFSINFNITKDRFAELLALESEAGVPALVGPSAFKIPFLIRQKIIS 480
Qy      823 LDPPCRRGADWRTLAQKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAVAG 882
Db      481 LDPPCRRGADWRTLAQKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAVAG 540
Qy      883 LGQPDAGLFT-VSEAE 898
Db      541 TXPAGRWLLSQCSEAE 557

```

RESULT 12

US-09-970-944-15

; Sequence 15, Application US/09970944

; Publication No. US20030204052A1

; GENERAL INFORMATION:

; APPLICANT: Herrman, John L

; APPLICANT: Rastelli, Luca

; APPLICANT: Shimkets, Richard A

; TITLE OF INVENTION: No. US20030204052A1e1 Proteins and Nucleic Acids Encoding Same and

; TITLE OF INVENTION: Antibodies Directed Against these Proteins

; FILE REFERENCE: 21402-138

; CURRENT APPLICATION NUMBER: US/09/970,944

; CURRENT FILING DATE: 2002-05-02

; PRIOR APPLICATION NUMBER: 60/237,862

; PRIOR FILING DATE: 2000-10-04

; NUMBER OF SEQ ID NOS: 62

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 15

; LENGTH: 931

; TYPE: PRT

; ORGANISM: Caenorhabditis elegans

US-09-970-944-15

Query Match 58.2%; Score 2787; DB 11; Length 931;

Best Local Similarity 57.3%; Pred. No. 3.6e-231;

Matches 522; Conservative 153; Mismatches 208; Indels 28; Gaps 9;

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Qy      9 PALLGIVLAAWLRGSGAQQSA---TVANPVPGANPDLLPHFLVEPEDVYIVKNKPVLLVC 65
      ||| :|:| || || : | |: ||||:|:| ||||| | |
Db      26 PAL--ALLSASGTGSAAQDDEFFHELPETFPSPPEPLPHFLIEPEEAYIVKNKPVNLYC 83
Qy      66 KAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQQVEKVFGLLEEWYCQ 125
      || ||||:|:| || | |||: : | :|| | | :|||:|:| |:|:|
Db      84 KASPATQIYFKCNSEWVHQKDHVVDERVDSETSGLIVREVSIEISRQQVEELFGPEDYWCQ 143
Qy      126 CVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPGIPPAEVEWLR 185
      ||||:|:|:|:| || || |||| ||||| :| ||||| |||||:
Db      144 CVAWSSAGTTKSRKAYVRIAYLRKTFEQEPLGKEVSLEQEVLLQCRPPGIPVAEVEWLK 203
Qy      186 NEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAAVIVYVNGGW 245
      |||:|:| | | || :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      204 NEDIIDPAEDRNFYITIDHNLIIKQARLSDTANYTCVAKNIVAKRKSTTATVIVYVNGGW 263
Qy      246 STWTEWSVCSASCGRGWQKRSRSCNPNAPLNGGAFCEGQNVQKTACATLCPVDGSWSFWS 305

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Db	264	STWTEWSVCNSRCGRGYQKRTRTCTNPAPLNGGAFCEGQSVQKIAC TTLC PVDGRWTSWS	323
Qy	306	KWSACGLDCTHWSRECS DPAPRNGGEECQGTDL DTRNCTSDLCVHSASGPEDVALYVGL	365
Db	324	KWSTCGTECTHWRRECTAPAPKNGGKDCDGLVLQSKNCTDGLCMQAAPSDDDVALYVGI	383
Qy	366	-IAVAVCLVLLLLVLILVYCRKKEGLDSDVADSSILTS GFQPVSIKPSKADNPHLLTIQP	424
Db	384	VIAVTVCLAITVVVALFVYRKNHRDFESDIIDSSALNGGFQPVNIKAARQD---LLAVPP	440
Qy	425	DLSTTTTTYQGS LCP RQDGPSPKFQLTNGHLLSPLGGGRHTLHHSS----PTSEAEFFVS	480
Db	441	DLTSAAAMYRGFPVYALHD-VSDKIPMTNSPILDPLPNLKIKVYNSSGAVTPQDDLAEFSS	499
Qy	481	RLS---TQNYF-----RSLPRGT--SNMTYGT FNFLGGR LMI PNTGISLLIPDAI	526
Db	500	KLSPQMTQSLLENEALNLKNQSLARQTDPSCTAFGT FNSLGGHLIIPNSGVSLIPAGAI	559
Qy	527	PRGKIYEIYLT LHKPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSDPS	586
Db	560	PQGRVYEMYVTVHRKENMRPPMEDSQTLLTPVVS CGPPGALLTRPVILT LHHCADPSTED	619
Qy	587	WSLR LKKQSCEGSWEDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVA	646
Db	620	WKIQLKNQAVQGWEDVVVVGEENFTTPCYIQLDAEACHILTENLSTYALVGQSTTKAAA	679
Qy	647	KRLKLLLFAPVACTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYH	706
Db	680	KRLKLAIFGPLCCSSLEYSIRVYCLDDTQDALKEVLQLERQMGQQLLEPKALHFKGSIH	739
Qy	707	NLRLSIHDVPSSLWKS KLLVS YQEIPFYHIWNGTQRYLHCTFTLERVSPSTS DLACKLWV	766
Db	740	NLRLSIHDIAHSLWKS KLLAKYQEIPFYHIWSGSQRNLHCTFTLERLSINTVELVCKLCV	799
Qy	767	WQVEGDGQSFSINFNITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKI ISSLDPP	826
Db	800	RQVEGEGQIFQLNCTVSEPTGIDLPLLDPASTITVTGPSAFSIP LPIRQKLCSSLDAP	859
Qy	827	CRRGADWRTLAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQP	886
Db	860	QTRGHDWRMLAHKLNLD RYLN YFATKSSPTGVILD LWEAQNFDPGNLSMLAAVLEEMGRH	919
Qy	887	DAGLFTVSEAE	897
Db	920	ETVVSLAAEGQ	930

RESULT 13

US-10-087-684-35

; Sequence 35, Application US/10087684

; Publication No. US20040029116A1

; GENERAL INFORMATION:

; APPLICANT: Edinger, Shlomit R.
 ; APPLICANT: MacDougall, John R.
 ; APPLICANT: Millet, Isabelle
 ; APPLICANT: Ellerman, Karen

; APPLICANT: Stone, David J.
 ; APPLICANT: Grosse, William M.
 ; APPLICANT: Lepley, Denise M.
 ; APPLICANT: Rieger, Daniel K.
 ; APPLICANT: Burgess, Cathereine E.
 ; APPLICANT: Casman, Stacie, J.
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Boldog, Ferenc L.
 ; APPLICANT: Li, Li
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Mishra, Vishnu
 ; APPLICANT: Shenoy, Suresh G.
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Tchernev, Velizar T.
 ; APPLICANT: Vernet, Corine A.M.
 ; APPLICANT: Zerhusen, Bryan D.
 ; APPLICANT: Malyankar, Uriel M.
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Miller, Charles E.
 ; APPLICANT: Gangolli, Esha A.
 ; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
 ; FILE REFERENCE: 21402-214 CIP
 ; CURRENT APPLICATION NUMBER: US/10/087,684
 ; CURRENT FILING DATE: 2003-03-10
 ; PRIOR APPLICATION NUMBER: 60/253,834
 ; PRIOR FILING DATE: 2000-11-29
 ; PRIOR APPLICATION NUMBER: 60/250,926
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: 60/264,180
 ; PRIOR FILING DATE: 2001-01-25
 ; PRIOR APPLICATION NUMBER: 60/274,194
 ; PRIOR FILING DATE: 2001-03-08
 ; PRIOR APPLICATION NUMBER: 60/313,656
 ; PRIOR FILING DATE: 2001-08-20
 ; PRIOR APPLICATION NUMBER: 60/327,456
 ; PRIOR FILING DATE: 2001-10-05
 ; NUMBER OF SEQ ID NOS: 220
 ; SOFTWARE: CuraSeqList version 0.1
 ; SEQ ID NO 35
 ; LENGTH: 931
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-087-684-35

Query Match 58.2%; Score 2787; DB 12; Length 931;
 Best Local Similarity 57.3%; Pred. No. 3.6e-231;
 Matches 522; Conservative 153; Mismatches 208; Indels 28; Gaps 9;

Qy 9 PALLGIVLAAWLRGSGAQQSA---TVANPVPGANPDLLPHFLVEPEDVYIVKNKPVLLVC 65
 ||| :|:| || || : | |: ||||:|:|: ||||| | |
 Db 26 PAL--ALLSASGTGSAAQDDEFFHELPETFPSDPPEPLPHFLIEPEEAYIVKNKPVNLYC 83
 Qy 66 KAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQQVEKVFGLLEEYWCQ 125
 || ||||:|:| || | ||:: | :|| || | :|||:|:| |:|:| |
 Db 84 KASPATQIYFKCNSEWVHQKDHVVDERVDETSGLIVREVSIEISRQQVEELFGPEDYWCQ 143
 Qy 126 CVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPPEGIPPAEVEWLR 185

Db	144	CVAWSSAGTTKSRKAYVRIAYLRKTFEQEPLGKEVSLEQEVLLQCRPPEGIPVAEVEWLK	203
Qy	186	NEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAAVIVYVNGGW	245
Db	204	NEDIIDPAEDRNFYITIDHNLIIKQARLSDTANYTCVAKNIVAKRKSTTATVIVYVNGGW	263
Qy	246	STWTEWSVCSASCGRGWQKRSRSCNTPAPLNGGAFCEGQNVQKTACATLCPVDGWSWPWS	305
Db	264	STWTEWSVCNSRCGRGYQKRTRCTNPAPLNGGAFCEGQSVQKIACTTLCPCVDGRWTSWS	323
Qy	306	KWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDRNCTSDLCVHSASGPEDVALYVGL	365
Db	324	KWSTCGTECTHWRRECTAPAPKNGGKDCDGLVLQSKNCTDGLCMQAAPSDDDVALYVGI	383
Qy	366	-IAVAVCLVLLLLVLILVYCRKKEGLSDSDVADSSILTSGFQPVSIKPSKADNPHELLTIQP	424
Db	384	VIAVTVCLAITVVVALFVYRKNHRDFESDIISSALNGGFQPVNIKAARQD---LLAVPP	440
Qy	425	DLSTTTTTTYQGLCPRQDGPSPKFQLTNGHLLSPLGGGRHTLHHSS---PTSEAEFEVS	480
Db	441	DLTSAAAMYRGPVYALHD-VSDKIPMTNSPILDPLPNLKI KVNSSGAVTPQDDLAEFSS	499
Qy	481	RLS---TQNYF-----RSLPRGT--SNMTYGTFFNLGGRLMIPNTGISLLIPPDAI	526
Db	500	KLSPQMTQSLLENEALNLKNQSLARQTDPSCTAFGTFFNSLGGHLIIPNSGVSLIPAGAI	559
Qy	527	PRGKIYEIYLT LHKPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSDPS	586
Db	560	PQGRVYEMYVTVHRKENMRPPMEDSQTLLTPVVSCGPPGALLTRPVILT LHHCADPSTED	619
Qy	587	WSRLRKKQSCEGSWEDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVAAA	646
Db	620	WKIQ LKNQAVQGWEDVVVGEENFTTPCYIQLDAEACHILTENLSTYALVGQSTTKAAA	679
Qy	647	KRLKLLLFAPVACTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYH	706
Db	680	KRLKLAIFGPLCCSSLEYSIRVYCLDDTDQDALKEVLQLERQMGGQLLEEPKALHFKGSIH	739
Qy	707	NLRLSIHDVPSSLWKSLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSD LACKLWV	766
Db	740	NLRLSIHDIAHSLWKSLLAKYQEIPFYHIWSGSQRN LHCTFTLERLSLNTVELVCKLCV	799
Qy	767	WQVEGDGQSFSINFNITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISSLDPP	826
Db	800	RQVEGEGQIFQLNCTVSEETGIDPLLLDPASTITVTGPSAFSIPLRQKLCSSLDAP	859
Qy	827	CRRGADWRTL AQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQP	886
Db	860	QTRGHDWRMLAHKLNLDRLNYFATKSSPTGVILDLWEAQNFDPGNLSMLAAVLEEMGRH	919
Qy	887	DAGLFTVSEAE	897
Db	920	ETVVS LAAEGQ	930

US-09-972-211-121
; Sequence 121, Application US/09972211
; Publication No. US20040048245A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Spytek, Kimberly Ann
; APPLICANT: Li, Li
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John R
; APPLICANT: Gunther, Erik
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David J
; APPLICANT: Smithson, Glennnda
; APPLICANT: Szekeres Jr, Edward S
; TITLE OF INVENTION: No. US20040048245A1el Human Proteins, Polynucleotides
Encoding Them And
; TITLE OF INVENTION: Methods Of Using The Same
; FILE REFERENCE: 21402-141
; CURRENT APPLICATION NUMBER: US/09/972,211
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,325
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,323
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,400
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,397
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,401
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,379
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,402
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 30/238,384
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,373
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,372
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,383
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,382
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/275,892
; PRIOR FILING DATE: 2001-03-14

; PRIOR APPLICATION NUMBER: 60/296,860
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 121
; LENGTH: 931
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-972-211-121

Query Match 58.2%; Score 2787; DB 12; Length 931;
Best Local Similarity 57.3%; Pred. No. 3.6e-231;
Matches 522; Conservative 153; Mismatches 208; Indels 28; Gaps 9;

Qy 9 PALLGIVLAAWLRGSGAQQSA---TVANPVPGANPDLLPHFLVEPEDVYIVKNKPVLLVC 65
||| :|| || | : | : ||||:||||: ||||| | |
Db 26 PAL--ALLSASGTGSAAQDDEFFHELPETFPSDPPEPLPHFLIEPEEAYIVKNKPVNLYC 83

Qy 66 KAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSROQVEKVFGLLEEYWCQ 125
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Qy 126 CVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPEGIPPAEVEWLR 185
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Db 204 NEDIIDPAEDRNFYITIDHNLIIKQARLSDTANYTCVAKNIVAKRKSTTATVIVYVNGGW 263

Qy 246 STWTEWSVCSASCGRGWQKRSRSTCTNPAPLNGGAFCEGQNVQKTACATLCPVDGSWSPWS 305
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Qy 306 KWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDRNCTSDLCVHSASGPEDVALYVGL 365
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Db 384 VIAVTVCLAITVVVALFVYRKNHRDFESDIIDSSALNGGFQPVNIKAARQD---LLAVPP 440

Qy 425 DLSTTTTTTYQGSCLCPQDGPSPKFQLTNGHLLSPLGGGRHTLHHSS----PTSEAEFVS 480
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Db 500 KLSPQMTQSLLENEALNLKNQSLARQTDPSCTAFGTENSLGGHLIIPNSGVSLIPAGAI 559

Qy 527 PRGKIYEIYLT LHKPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSDDS 586
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Db 560 PQGRVYEMYVTVHRKENMRPPMEDSQTLTPVTVSCGPPGALLTRPVILTLHHCADPSTED 619

Qy 587 WSLRLKKQSCGSEWEDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVA 646
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Db 620 WKIQLKNQAVQGQWEDVVVVGEEFTPCYIQLDAEACHILTENLSTYALVGQSTTKAAA 679


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; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 117
; LENGTH: 931
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-037-417-117

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Query Match          58.2%; Score 2787; DB 12; Length 931;
Best Local Similarity 57.3%; Pred. No. 3.6e-231;
Matches 522; Conservative 153; Mismatches 208; Indels 28; Gaps 9;

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Qy      9 PALLGIVLAAWLRGSGAQQSA---TVANPVPGANPDLLPHFLVEPEDVYIVKNKPVLLVC 65
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Db     26 PAL--ALLSASGTGSAAQDDEFFHELPETFSPDPPEPLPHFLIEPEEAYIVKNKPVNLYC 83

Qy     66 KAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQVEKVFGLLEEYWCQ 125
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Db     84 KASPATQIYFKCNSEWVHQKDHVVDERVEDTSGLIVREVSIIEISRQQVEELFGPEDYWCQ 143

Qy    126 CVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPEGIPPAEVEWLR 185
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Db    144 CVAWSSAGTTKSRKAYVRIAYLRKTTFQEPLGKEVSLEQEVLLQCRPPEGIPVAEVEWLK 203

Qy    186 NEDLVDPSPDPNVYITREHSIVVRQARLADTANYTCVAKNIVARRRSASAAVIVYVNGGW 245
      |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db    204 NEDIIDPAEDRNFYITIDHNLIIKQARLSDTANYTCVAKNIVAKRKSTTATVIVYVNGGW 263

Qy    246 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLCPVDGWSWPWS 305
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Db    264 STWTEWSVCNSRCGRGYQKRTRTCTNPAPLNGGAFCEGQSVQKIACTTLCVPDGRWTSWS 323

Qy    306 KWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDRNCTSDLCVHSASGPEDVALYVGL 365
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Db    324 KWSTCGTECTHWRRECTAPAPKNGGKDCDGLVLQSKNCTDGLCMQAAPSDDDVALYVGI 383

Qy    366 -IAVAVCLVLLLLVLILVYCRKKEGLSDVDSSILTSQFQPVSIKPSKADNPHLLTIQP 424
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Db    384 VIAVTVCLAITVVVALFVYRKNHRDFESDIIDSSALNGGFQPVNIKAARQD---LLAVPP 440

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 6, 2004, 14:29:11 ; Search time 49 Seconds
(without alignments)
5782.354 Million cell updates/sec

Title: US-10-624-932-2
Perfect score: 4791
Sequence: 1 MAVRPGWLWPALLGIVLAAWL.....AVAGLGQPDAGLFTVSEAE 898

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertibrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match	Length	DB	ID	Description

1	4685	97.8	898	11	Q8K1S4	Q8k1s4 mus musculu
2	4638	96.8	898	11	O08721	O08721 rattus norv
3	2845	59.4	544	4	Q96GP4	Q96gp4 homo sapien
4	2787	58.2	931	11	O08747	O08747 mus musculu
5	2767.5	57.8	950	11	Q8CD16	Q8cd16 mus musculu
6	2761	57.6	931	13	Q7T2Z5	Q7t2z5 gallus gall
7	2755	57.5	931	4	O95185	O95185 homo sapien
8	2646.5	55.2	943	13	Q8JGT4	Q8jgt4 xenopus lae
9	2585	54.0	1008	11	Q80Y85	Q80y85 mus musculu
10	2578.5	53.8	945	11	Q8K1S3	Q8k1s3 mus musculu
11	2578.5	53.8	945	11	O08722	O08722 rattus norv
12	2572.5	53.7	945	11	Q9D398	Q9d398 mus musculu
13	2566	53.6	934	4	Q8IZJ1	Q8izj1 homo sapien
14	2558.5	53.4	945	4	Q86SN3	Q86sn3 homo sapien
15	2200	45.9	956	11	Q8K1S2	Q8k1s2 mus musculu
16	2189.5	45.7	948	4	Q8WYP7	Q8wyp7 homo sapien
17	1668.5	34.8	597	4	Q8IUT0	Q8iut0 homo sapien
18	1458	30.4	328	11	Q80T71	Q80t71 mus musculu
19	1242.5	25.9	554	4	Q8N1Y2	Q8nly2 homo sapien
20	997	20.8	1072	5	Q9NBL0	Q9nbl0 drosophila
21	992	20.7	1072	5	Q9V7B5	Q9v7b5 drosophila
22	981.5	20.5	366	4	Q9H9F3	Q9h9f3 homo sapien
23	980	20.5	947	5	Q26262	Q26262 caenorhabdi
24	977	20.4	947	5	O44171	O44171 caenorhabdi
25	692	14.4	199	13	Q9PVD5	Q9pvd5 petromyzon
26	552.5	11.5	351	4	Q8TF26	Q8tf26 homo sapien
27	377.5	7.9	2673	4	Q96SC3	Q96sc3 homo sapien
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29	318	6.6	325	5	Q8I1K1	Q8il1k1 drosophila
30	300	6.3	518	4	Q8IV45	Q8iv45 homo sapien
31	293	6.1	1172	11	Q8CG21	Q8cg21 mus musculu
32	293	6.1	1172	11	Q7TMT3	Q7tmt3 mus musculu
33	292	6.1	1582	11	Q8CGM0	Q8cgm0 mus musculu
34	286	6.0	1081	5	Q9U631	Q9u631 drosophila
35	285	5.9	1083	5	Q9VTT0	Q9vtt0 drosophila
36	285	5.9	1091	5	Q7YU67	Q7yu67 drosophila
37	276	5.8	1461	5	Q8MYA8	Q8mya8 caenorhabdi
38	275.5	5.8	1122	11	Q7TT33	Q7tt33 mus musculu
39	275	5.7	1522	11	Q80ZF8	Q80zf8 mus musculu
40	274.5	5.7	1573	4	Q8NGW8	Q8ngw8 homo sapien
41	273.5	5.7	478	11	Q8BVE5	Q8bve5 mus musculu
42	271.5	5.7	685	6	Q9TTS5	Q9tts5 bos taurus
43	271.5	5.7	5146	6	Q8SPM4	Q8spm4 bos taurus
44	271	5.7	1560	11	Q8CGM1	Q8cgm1 mus musculu
45	270.5	5.6	1171	11	Q8CGB2	Q8cgb2 mus musculu

ALIGNMENTS

RESULT 1

Q8K1S4

ID Q8K1S4 PRELIMINARY; PRT; 898 AA.

AC Q8K1S4;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Netrin receptor Unc5h1.
 GN UNC5H1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Engelkamp D.;
 RT "Cloning of three mouse unc-5 genes and their expression patterns at
 RT mid-gestation.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ487852; CAD32250.1; -.
 DR MGD; MGI:894682; Unc5h1.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; tsp_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Receptor.
 SQ SEQUENCE 898 AA; 98856 MW; 59F04BA2E196C1DB CRC64;

Query Match 97.8%; Score 4685; DB 11; Length 898;
 Best Local Similarity 96.7%; Pred. No. 0;
 Matches 868; Conservative 19; Mismatches 11; Indels 0; Gaps 0;

Qy	1	MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP	60
Db	1	MAVRPGLWPALLGIVLTAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP	60
Qy	61	VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRQQVEKVFGL	120
Db	61	VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRQQVEKVFGL	120
Qy	121	EYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPGIPP	180
Db	121	EYWCQCVAWSSSGTTKSQKAYIRIAYLRKNFEQEPLAKEVSLEQGIVLPCRPPGIPP	180
Qy	181	VEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASA	240
Db	181	VEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASA	240
Qy	241	VNGGWSTWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLCPVD	300

Db	241	VNGGWSTWTEWSVCSASCGRGWQKRSRSCCTNPAPLNGGAFCEGQNVQKTACATLC PVDGS	300
Qy	301	WSPWSKWSACGLDCTHWSRECSDFAPRNGGEECQGTDLDTNRCTSDLCVHSASGPEDVA	360
Db	301	WSPWSKWSACGLDCTHWSRECSDFAPRNGGEECRGADLDTRNCTSDLC LHTSSGPEDVA	360
Qy	361	LYVGLIAVAVCLVLLLLVLILVYCRKKEGLDSDVADSSILTS GFQPVS IKPSKADNPHLL	420
Db	361	LYIGLVAVAVCLILLLLLVLVLIYCRKKEGLDSDVADSSILTS GFQPVS IKPSKADNPHLL	420
Qy	421	TIQPDLS TTTT TYQGS LCPRQDGPSPK FQLTNGHLLSPLGGGRHTLHHSSPTSEAEFVS	480
Db	421	TIQPDLS TTTT TYQGS LCPRQDGPSPK FQLSNGHLLSPLGSGRHTLHHSSPTSEAEFVS	480
Qy	481	RLSTQNYFRSLPRGTSNM TYGT FNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLT LHK	540
Db	481	RLSTQNYFRSLPRGTSNMAYGT FNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLT LHK	540
Qy	541	PEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPD SWSLRLKKQSCEGSW	600
Db	541	PEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPD SWSLRLKKQSCEGSW	600
Qy	601	EDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVA AAKRLKLLLFAPVACT	660
Db	601	EDVLHLGEESPSHLYYCQLEAGACYVFTEQLGRFALVGEALSVA ATKRLRLLLFAPVACT	660
Qy	661	SLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIH DVPSSLW	720
Db	661	SLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIH DVPSSLW	720
Qy	721	KSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSD LACKLWVWQVEGDGQSFSINF	780
Db	721	KSKLLVSYQEIPFYHIWNGTQQYLHCTFTLERVNA STDLACKVWVWQVEGDGQSFNINF	780
Qy	781	NITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIIS SLDPPCR RGADWRTLAQKL	840
Db	781	NITKDTRFAEMLALESEGGVPALVGPSAFKIPFLIRQKIITSLDPPCSRGADWRTLAQKL	840
Qy	841	HLDSHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAVAGLGQPDAGLFTVSEAEC	898
Db	841	HLDSHLSFFASKPSPTAMILNLWEARHFPNGNLGQLAAVAGLGQPDAGLFTVSEAEC	898

RESULT 2

O08721

ID O08721 PRELIMINARY; PRT; 898 AA.

AC O08721;

DT 01-JUL-1997 (TrEMBLrel. 04, Created)

DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Transmembrane receptor UNC5H1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Ventral spinal cord;
 RX MEDLINE=97271897; PubMed=9126742;
 RA Leonardo E.D., Hinck L., Masu M., Keino-Masu K., Ackerman S.L.,
 RA Tessier-Lavigne M.;
 RT "Vertebrate homologues of C. elegans UNC-5 are candidate netrin
 RT receptors.";
 RL Nature 386:833-838(1997).
 DR EMBL; U87305; AAB57678.1; -.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; tsp_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Receptor.
 SQ SEQUENCE 898 AA; 98840 MW; 7A3CBCB9E7ACA135 CRC64;

Query Match 96.8%; Score 4638; DB 11; Length 898;
 Best Local Similarity 96.0%; Pred. No. 0;
 Matches 862; Conservative 17; Mismatches 19; Indels 0; Gaps 0;

Qy	1	MAVRPGLWPALIGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP	60
Db	1	MAVRPGLWPVLLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP	60
Qy	61	VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSQQVEKVFGL	120
Db	61	VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDSSGLPTMEVRINVSQQVEKVFGL	120
Qy	121	EYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPEGIPPAE	180
Db	121	EYWCQCVAWSSSGTTKSQKAYIRIAYLRKNFEQEPLAKEVSLEQGIVLPCRPPEGIPPAE	180
Qy	181	VEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAIVY	240
Db	181	VEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSTSAIVY	240
Qy	241	VNGGWSTWTEWSVCSASCGRGWQKRSRSCNTPAPLNGGAFCEGQNVQKTACATLCPVDGS	300
Db	241	VNGGWSTWTEWSVCSASCGRGWQKRSRSCNTPAPLNGGAFCEGQNVQKTACATLCPVDGS	300
Qy	301	WSPWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDTNRNCTSDLCVHSASGPEDVA	360

DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00791; ZU5; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00218; ZU5; 1.
 KW Receptor; Transmembrane.
 FT NON_TER 1 1
 SQ SEQUENCE 544 AA; 59949 MW; 350A7BA53375CCAE CRC64;

Query Match 59.4%; Score 2845; DB 4; Length 544;
 Best Local Similarity 100.0%; Pred. No. 1.9e-253;
 Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	358	DVALYVGLIAVAVCLVLLLLVLILVYCRKKEGLDSDVADSSILTSGFQPVSIKPSKADNP	417
Db	4	DVALYVGLIAVAVCLVLLLLVLILVYCRKKEGLDSDVADSSILTSGFQPVSIKPSKADNP	63
Qy	418	HLLTIQPDLSSTTTTYQGSLCPRQDGPSPKFQLTNGHLLSPLGGGRHTLHHSSPTSEAAE	477
Db	64	HLLTIQPDLSSTTTTYQGSLCPRQDGPSPKFQLTNGHLLSPLGGGRHTLHHSSPTSEAAE	123
Qy	478	FVSRLSTQNYFRSLPRGTSNMTYGTFFNLGGRLMIPNTGISLLIPPDAIPRGIYEIYLT	537
Db	124	FVSRLSTQNYFRSLPRGTSNMTYGTFFNLGGRLMIPNTGISLLIPPDAIPRGIYEIYLT	183
Qy	538	LHKPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDWSLRLKKQSCE	597
Db	184	LHKPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDWSLRLKKQSCE	243
Qy	598	GSWEDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVAAPKRLKLLLFAPV	657
Db	244	GSWEDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVAAPKRLKLLLFAPV	303
Qy	658	ACTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPS	717
Db	304	ACTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPS	363
Qy	718	SLWKSLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFS	777
Db	364	SLWKSLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFS	423
Qy	778	INFNITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISLDPPCRRGADWRTLA	837
Db	424	INFNITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISLDPPCRRGADWRTLA	483
Qy	838	QKLHLDSHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAE	897
Db	484	QKLHLDSHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAE	543
Qy	898	C	898
Db	544	C	544

RESULT 4

O08747

ID O08747 PRELIMINARY; PRT; 931 AA.
 AC O08747;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Rostral cerebellar malformation protein.
 GN UNC5H3 OR RCM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57B6/SJL;
 RX MEDLINE=97271898; PubMed=9126743;
 RA Ackerman S.L., Kozak L.P., Przyborski S.A., Rund L.A., Boyer B.B.,
 RA Knowles B.B.;
 RT "The mouse rostral cerebellar malformation gene encodes an UNC-5-like
 RT protein.";
 RL Nature 386:838-842(1997).
 DR EMBL; U72634; AAB54103.1; -.
 DR MGD; MGI:1095412; Unc5h3.
 DR GO; GO:0005886; C:plasma membrane; IC.
 DR GO; GO:0005042; F:netrin receptor activity; IDA.
 DR GO; GO:0005515; F:protein binding; IDA.
 DR GO; GO:0007420; P:brain development; IMP.
 DR GO; GO:0030334; P:regulation of cell migration; IMP.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; tsp_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 931 AA; 103062 MW; 8A5D951A4EECA179 CRC64;

Query Match 58.2%; Score 2787; DB 11; Length 931;
 Best Local Similarity 57.3%; Pred. No. 9.7e-248;
 Matches 522; Conservative 153; Mismatches 208; Indels 28; Gaps 9;

Qy 9 PALLGIVLAAWLRGSGAQQSA---TVANVPVPGANPDLLPHFLVEPEDVYIVKNKPVLLVC 65
 ||| :|:| || || : | |: ||||:|:|: ||||| | |
 Db 26 PAL--ALLSASGTGSAAQDDEFFHELPETFPSDPPEPLPHFLIEPEEAYIVKNKPVNLYC 83

Qy	66	KAVPATQIFFKCNSEWVHQVDHVIERSTDGSSGLPTMEVRINRSRQQVEKVFGLLEEYWCQ	125
Db	84	KASPATQIYFKCNSEWVHQDHDVDERVDETSGLIVREVSIETSRQQVEELFGPEDYWCQ	143
Qy	126	CVAWSSSGTTKSKQAYIRIARLRKNFEQEPLAKEVSLEQGIIVLPCRPPGIPPAEVEWLR	185
Db	144	CVAWSSAGTTKSRKAYVRIAYLRKTFEQEPLGKEVSLEQEVLLQCRPPGIPVAEVEWLK	203
Qy	186	NEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAAVIVYVNGGW	245
Db	204	NEDIIDPAEDRNFYITIDHNLIIKQARLSDTANYTCVAKNIVAKRKSTTATVIVYVNGGW	263
Qy	246	STWTEWSVCSASCGRGWQKRSRSCCTNPAPLNGGAFCEGQNVQKTACATLCPVDGSWSPWS	305
Db	264	STWTEWSVCNSRCGRGYQKRTRCTNPAPLNGGAFCEGQSVQKIACTTLCVPDGRWTSWS	323
Qy	306	KWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDRNCTSDLCVHSASGPEDVALYVGL	365
Db	324	KWSTCGTECTHWRRECTAPAPKNGGKDCDGLVLQSKNCTDGLCMQAAPDSDDVALYVGI	383
Qy	366	-IAVAVCLVLLLLVLILVYCRKKEGLSDSDVADSSIITSGFQPVSIKPSKADNPHLLTIQP	424
Db	384	VIAVTVCLAITVVVALFVYRKNHRDFESDIIDSSALNGGFQPVNIKAARQD---LLAVPP	440
Qy	425	DLSTTTTTYQGSILCPQDGPSPKFQLTNGHLLSPLGGGRHTLHHSS---PTSEAEFVS	480
Db	441	DLTSAAAMYRGFPVYALHD-VSDKIPMTNSPILDPLPNLKIKVYNSSGAVTPQDDLAEFSS	499
Qy	481	RLS---TQNYF-----RSLPRGT--SNMTYGTNFNLGGRLMIPNTGISLLIPDAI	526
Db	500	KLSPQMTQSLLENEALNLKNQSLARQTDPSCTAFGTFSNLGGHLIIPNSGVSLIPAGAI	559
Qy	527	PRGKIYEIYLTTLHKPEDVRLPLAGCQTLTSPIVSCGPPGVLLTRPVILAMDHCGEPSDPS	586
Db	560	PQGRVYEMYVTVHRKENMRPPMEDSQTLTTPVVSCTGPPGALLTRPVILTTLHHCADPSTED	619
Qy	587	WSLRLKKQSCEGSWEDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVA	646
Db	620	WKIQLKNAQVQGWEDVVVVGEENFTTPCYIQLDAEACHILTENLSTYALVGQSTTKAAA	679
Qy	647	KRLKLLLFAPVACTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYH	706
Db	680	KRLKLAIFGPLCCSSLEYSIRVYCLDDTDALKEVLQLERQMGQQLLEEPKALHFKGSIH	739
Qy	707	NLRLSIHDVPSLWKSLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWV	766
Db	740	NLRLSIHDIASHLWKSLLAKYQEIPFYHIWSGSQRLHCTFTLERLSLNTVELVCKLCV	799
Qy	767	WQVEGDGQSFSINFNITKDTRFAELLALESEAGVPALVGPSPAFKIPFLIRQKIISLDP	826
Db	800	RQVEGEGQIFQLNCTVSEETPIDLPLLDPASTITVTGSPAFSIPPIRQKLCSSLDAP	859
Qy	827	CRRGADWRTLQAKLHLDHLSFFASKPSPTAMILNLWEARHPNGNLSQLAAAVAGLGQP	886
Db	860	OTRGHDWRMLAHKLNLDRLNYFATKSSPTGVILDLWEAQNFDPGNLSMLAAVLEEMGRH	919

Qy 887 DAGLFTVSEAE 897
 : : :| :
Db 920 ETVVSLAAEQ 930

RESULT 5

Q8CD16

ID Q8CD16 PRELIMINARY; PRT; 950 AA.
AC Q8CD16;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Unc5 homolog.
GN UNC5H3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK031655; BAC27495.1; -.
DR PIR; PT0566; PT0566.
DR MGD; MGI:1095412; Unc5h3.
DR GO; GO:0005886; C:plasma membrane; IC.
DR GO; GO:0005042; F:netrin receptor activity; IDA.
DR GO; GO:0005515; F:protein binding; IDA.
DR GO; GO:0007420; P:brain development; IMP.
DR GO; GO:0030334; P:regulation of cell migration; IMP.
DR InterPro; IPR000488; Death.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR InterPro; IPR000906; ZU5.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00090; tsp_1; 2.
DR Pfam; PF00791; ZU5; 1.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGc2; 1.
DR SMART; SM00209; TSP1; 2.
DR SMART; SM00218; ZU5; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50092; TSP1; 2.
SQ SEQUENCE 950 AA; 105398 MW; 1E8FC74703351AF6 CRC64;

Query Match 57.8%; Score 2767.5; DB 11; Length 950;

Best Local Similarity 56.1%; Pred. No. 6.3e-246;
Matches 522; Conservative 153; Mismatches 208; Indels 47; Gaps 10;

Qy 9 PALLGIVLAAWLRGSGAQQA---TVANPVPGANPDLLPHFLVEPEDVYIVKNKPVLLVC 65
||| :|| | | | : | | : ||||| :||| : ||||| | |
Db 26 PAL--ALLSASGTGSAAQDDEFFHELPETFPSPDPPEPLPHFLIEPEEAYIVKNKPVNLYC 83

Qy 66 KAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQQVEKVFGLEEYWCQ 125
|| ||||| :||| | | | | : | :|| | | | :||| :||| :|||
Db 84 KASPATQIYFKCNSEWVHQKDHVVDERVDETSGLIVREVSIEISRQQVEELFGPEDYWCQ 143

Qy 126 CVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPEGIPPAEVEWLR 185
||| :||| :||| :||| | | | | | | | | :| | | | | | | | :||| :||| :|||
Db 144 CVAWSSAGTTKSRKAYVRIAYLRKTFEQEPLGKEVSLEQEVLLQCRPPEGIPVAEVEWLK 203

Qy 186 NEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAAVIVYVNGGW 245
||| :||| : | | | | :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 204 NEDIIDPAEDRNFYITIDHNLIIKQARLSDTANYTCVAKNIVAKRKSTTATVIVYVNGGW 263

Qy 246 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLCPVDGWSWPWS 305
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 264 STWTEWSVCNSRCGRGYQKRTRCTNPAPLNGGAFCEGQSVQKIACTTLCVPDGRWTSWS 323

Qy 306 KWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDRNCTSDLCVH----- 351
||| | | :||| | | : ||| :||| :||| :||| :||| :||| :||| :|||
Db 324 KWSTCGTECTHWRRECTAPAPKNGGKDCDGLVLQSKNCTDGLCMQGGFIYPISTEHRPQN 383

Qy 352 -----SASGPEDVALYVGL-IAVAVCLVLLLLVLILVYCRKKEGLDSDVADSSILTSGFQ 405
| | :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 384 EYGFSSAPDSDDVALYVGIVIAVTVCLAITVVVALFVYRKNHRDFESDIIDSSALNGGFQ 443

Qy 406 PVSIIKPSKADNPHLLTIQPDLTSTTTTYQGSILCPQDGPSPKFQLTNGHLLSPLGGGRHT 465
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 444 PVNIKAARQD---LLAVPPDLTSAAMYRGFPVYALHD-VSDKIPMTNSPILDPLPNLKIK 499

Qy 466 LHHSS----PTSEAEFFVSRLS---TQNYF-----RSLPRGT--SNMTYGTENFLG 507
: :||| | : | | | | :||| :||| :||| :||| :||| :||| :||| :|||
Db 500 VYNSSGAVTPQDDLAEFSSKLSPQMTQSLLENEALNLKNQSLARQTDPSCTAFGTENSLG 559

Qy 508 GRLMIPNTGISLLIPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTLSPIVSCGPPGVL 567
| | :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 560 GHIIIPNSGVSLIPAGAIPOGRVYEMYVTVHRKENMRPPMEDSQTLTPVVSCTGPPGAL 619

Qy 568 LTRPVILAMDHCGEPSDWSLRLKKQSCGWSWEDVLHLGEEAPSHLYYCQLEASACYVF 627
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 620 LTRPVILTLLHCADPSTEDWKIQLKNQAVQGWEDVVVVGEENFTTPCYIQLDAEACHIL 679

Qy 628 TEQLGRFALVGEALSVAALKRLKLLLFAPVACTSLEYNIRVYCLHDTHDALKEVVQLEKQ 687
|| | :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 680 TENLSTYALVGQSTTKAAAKRLKLAIFGFLCCSSLEYSIRVYCLDDTQDALKEVLQLERQ 739

Qy 688 LGGQLIQEPRVLHFKDSYHNLRLSIHDPSSSLWKSLLVSYQEIPFYHIWNGTQRYLHCT 747
:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 740 MGGQLLEPKALRFKGSIHNLRLSIHDIAHSLWKSLLAKYQEIPFYHIWSGSQRNHCT 799

Qy 748 FTLERVSPSTSDLACKLWVWQVEGDGQSFSINFNITKDTRFAELLALESEAGVPALVGPS 807
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Db 800 FTLERLSLNTVELVCKLCVRQVEGEGQIFQLNCTVSEEPTGIDLPLLDPASTITVTGPS 859

Qy 808 AFKIPFLIRQKIISSLDPPCRRGADWRTLAQKLHLDSHLSFFASKPSPTAMILNLWEARH 867
 || || ||||: |||| | || ||| || ||: || | |: ||: || | || | : ||: ||||: :

Db 860 AFSIPLPIRQKLCSSLDAPQTRGHDWRMLAHKLNLDRLNYFATKSSPTGVILDLWEAQN 919

Qy 868 FPNGNLSQLAAAVAGLGQPDAGLFTVSEAE 897
 ||: |||| ||| : |: : :: :| :

Db 920 FPDGNLSMLAAVLEEMGRHETVVYLA AEGQ 949

RESULT 6

Q7T2Z5

ID Q7T2Z5 PRELIMINARY; PRT; 931 AA.

AC Q7T2Z5;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE UNC5-like protein 3.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RA Guan W., Condic M.L.;

RT "Characterization of Netrin-1, Neogenin and cUNC-5H3 expression during

RT chick dorsal root ganglia development.";

RL Gene Expr. Patterns 3:369-373(2003).

DR EMBL; AY187310; AA067275.1; -.

SQ SEQUENCE 931 AA; 102906 MW; 1E23A0D84F2E2C62 CRC64;

Query Match 57.6%; Score 2761; DB 13; Length 931;

Best Local Similarity 57.0%; Pred. No. 2.4e-245;

Matches 518; Conservative 151; Mismatches 212; Indels 28; Gaps 9;

Qy 9 PALLGIVLAAWLRGSGAQQS---ATVANPVPGANPDLLPHFLVEPEDVYIVKNKPVLLVC 65
 ||| || | || || : | |: ||||: ||: ||||| || |

Db 26 PAL--AVLGASRPGSAAQDDDFHELPETFPSPPEPLPHFLIEPEEAYIVKNKPVNLYC 83

Qy 66 KAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQVEKVFGLLEEWYCQ 125
 || ||||: |||| || | |||: : | : || | || | : ||||: || | : ||||

Db 84 KASPATQIYFKCNSEWVHQKDHVVDERVDETSGLIVCEVSIEISRQQVEELFGPEDYWCQ 143

Qy 126 CVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPEGIPPAEVEWLR 185
 |||||: ||||: ||: || || |||| ||||| :| ||||| |||||:

Db 144 CVAWSSAGTTKSRKAYVRIAYLRKTFEQEPLGKEVSLEQEVLLQCRPEGIPVAEVEWLK 203

Qy 186 NEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAIVIVVNGGW 245
 ||::: || | || | |: |: : ||||: ||||| |||||: |: | : ||||| ||

Db 204 NEEVIDPVEDRNFYITIDHNLIIKQARLSDTANYTCVAKNIVAKRKSTTATVIVVNGGW 263

Qy 246 STWTEWSVCSASCGRGWQKRSRSCINPAPLNGGAFCEGQNVQKTACATLCPVDGWSWPWS 305
 ||||| |: ||||: |||: |: ||||| ||||| || || ||||| |: ||

Db 264 STWTEWSACNSRCGRGFQKRTRTCTNPAPLNGGAFCEGQNVQKIACTTLCVPDGKWTWS 323

Qy 306 KWSACGLDCTHWRSRECS DPAPRNGGEECQGTDLDTNRCTSDLCVHSASGPEDVALYVGL 365
 ||| || :||| |||: |||:||||:|:| | :||| ||: :| :||| |||:
 Db 324 KWSTCGTECTHWRRRECTAPAPKNGGKDCEGLVLQSKNCTDGLCMQAAPSDSDVALYVGI 383

Qy 366 -IAVAVCLVLLLVLILVYCRKKEGLSDVADSSILTS GFQPVSIKPSKADNPHLLTIQP 424
 ||| ||| : :| : || : :||: ||| | ||||: || :| || : |
 Db 384 VIAVIVCLAISVVVALFVYRKNHRDFESDIIDSSALNGGFQPVNIKAARQD---LLAVPP 440

Qy 425 DLSTTTTTTYQGS LCPQDGPSPKFQLTNGHLLSPLGGGRHTLHHSS----PTSEAEFVS 480
 ||:: ||: | | | :|| :|| | : :::| | | :| |
 Db 441 DLTSAAAMYRGVPYALHD-VSDKIPMTNSPILDPLPNLKIKVYNTSGAVTPQDELSDFSS 499

Qy 481 RLS---TQNYF-----RSLPRGT--SNMTYGT FNFLGGRLMIPNTGISLLIPDAI 526
 :|| ||: :|| | | | :||| ||| |:|||:|:|||| |:
 Db 500 KLSPQITQS LLENETLNVKNQSLARQTDPSCTAFGT FNSLGGHLVIPNSGVSLIPAGAV 559

Qy 527 PRGKIYEIYLT LHKPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSDPS 586
 |:|::||:|:|:| | :| |: |||:|:||||| |||||:| | || |: |
 Db 560 PQGRVYEMYVTVHRKEGMRPPVEDSQTLLTPVVS CGPPGALLTRPVVLTMHHCAPNMDD 619

Qy 587 WSLRLKKQSCEGSWEDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVA 646
 | :|| | : :| ||||: :|| | : | ||: ||: || | :|||::: ||
 Db 620 WQIQLKHQAGQGPWEDVVVGEENFTTPCYIQLDPEACHILTETLSTYALVGQSITKAAA 679

Qy 647 KRLKLLLFPVACTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYH 706
 |||| :| |:|:|:|:|:| || |||||:|:|:|:|:|:|:| ||| | |
 Db 680 KRLKLAIFGPLSCSSLEYSIRVYCLDDTDALKEVLQLERQMGGQLLEPKTLHFKGSTH 739

Qy 707 NLRLSIHDVPSSLWKS KLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSD LACKLWV 766
 |||||: | ||||| |||||:| || ||||| | :| :| || |
 Db 740 NLRLSIHDIAHSLWKS KLPKYQEIPFYHIWSGCQRNLHCTFTLERFSLNTLELVCKLCV 799

Qy 767 WQVEGDGQSFSINFNITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKI ISSLDPP 826
 ||||:| | :| :::: : :| : :||:| || |||: ||| |
 Db 800 RQVEGEGQIFQLNCSVSEETGIDYPIMDSAGSITTIVGPNAFSIPLPIRQKLCSSLDAP 859

Qy 827 CRRGADWRTLAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQP 886
 || || | || | :|:|:| || | :|:|:|:|:|:| || | :|:
 Db 860 QTRGHDWRMLAHKLKLD RYLNYPATKSSPTGVILDLWEAQNFPDGNLSMLAAVLEEMGRH 919

Qy 887 DAGLFTVSE 895
 : : :|
 Db 920 ETVVSLAAE 928

RESULT 7

O95185

ID O95185 PRELIMINARY; PRT; 931 AA.

AC O95185;

DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Transmembrane receptor UNC5C.

GN UNC5C.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99000841; PubMed=9782087;
 RA Ackerman S.L., Knowles B.B.;
 RT "Cloning and mapping of the UNC5C gene to human chromosome 4q21-q23.";
 RL Genomics 52:205-208(1998).
 DR EMBL; AF055634; AAC67491.1; -.
 DR Genew; HGNC:12569; UNC5C.
 DR GO; GO:0005042; F:netrin receptor activity; TAS.
 DR GO; GO:0007411; P:axon guidance; TAS.
 DR GO; GO:0007420; P:brain development; TAS.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; tsp_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Immunoglobulin domain; Receptor.
 SQ SEQUENCE 931 AA; 103101 MW; EFD71122C98DABB8 CRC64;

Query Match 57.5%; Score 2755; DB 4; Length 931;
 Best Local Similarity 56.4%; Pred. No. 8.7e-245;
 Matches 514; Conservative 154; Mismatches 215; Indels 28; Gaps 9;

Qy	9	PALLGIVLAAWLRGSGAQQS---ATVANPVPGANPDLLPHFLVEPEDVYIVKKNKPVLLVC	65
		: : : : : : : : :	
Db	26	PAL--ALLSASGTGSAAQDDDFHHELPETFPSPDPEPLPHFLIEPEEAYIVKKNKPVNLYC	83
Qy	66	KAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQQVEKVFGLLEEWYCQ	125
		: : : :: : : : : : :	
Db	84	KASPATQIYFKCNSEWVHQKDHIVDERVDETSGLIVREVSIEISRQQVEELFGPEDYWCQ	143
Qy	126	CVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPGEGIPPAEVEWLIR	185
		: : : : : : : : : :	
Db	144	CVAWSSAGTTKSRKAYVRIAYLRKTFEQEPLGKEVSLEQEVLLQCRPPGEGIPVAEVEWLK	203
Qy	186	NEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAAVIVYVNGGW	245
		: : : : : : : : : : : : : : : : : :	
Db	204	NEDIIDPVEDRNFYITIDHNLIIKQARLSDTANYTCVAKNIVAKRKSTTATVIVYVNGGW	263
Qy	246	STWTEWSVCSASCGRGWQKRSRSCCTNPAPLNGGAFCEGQNVQKTACATLCPVDGSWSPWS	305
		: :	
Db	264	STWTEWSVCNSRCGRGYQKRTRTCTNPAPLNGGAFCEGQSVQKIACTTLCPVDGRWTPWS	323

Qy 306 KWSACGLDCTHWSRECS DPAPRNGGEECQGTDLDRNCTSDLCVHSASGPEDVALYVGL 365
 ||| || :||| |||: |||: |||: || | | :||| ||: :| :||| |||:
 Db 324 KWSTCGTECTHWRRECTAPAPKNGGKDCDGLVLQSKNCTDGLCMQTAPDSDDVALYVGI 383

Qy 366 -IAVAVCLVLLLLVLILVYCRKKEGLDSDVADSSILTS GFQPVSIKPSKADNPHELLTIQP 424
 ||| ||| : :| : || : :||: || | |||: || :| || : |
 Db 384 VIAVIVCLAISVVVALFVYRKNHRDFESDIIDSSALNGGFQPVNIKAARQD---LLAVPP 440

Qy 425 DLSTTTTTYQGS LCPQDGPSPKFQLTNGHLLSPLGGGRHTLHHS----SPTSEAEFEFVS 480
 ||: : ||: : | | | :|| :|| : : : : || : || |
 Db 441 DLTSAAAMYRGPVYALHD-VSDKIPMTNSPILDPLPNLKIKVYNTSGAVSPQDDLSEFTS 499

Qy 481 RLS---TQNYF-----RSLPRGT--SNMTYGT FNFLGGRLMIPNTGISLLIPDAI 526
 :|| ||: :|| | | | :|| || || :||: ||: |||| ||
 Db 500 KLS PQMTQS LLENEALSLKNQSLARQTDPSCTAFGSFNSLGGHLIVPNSGVSLIPAGAI 559

Qy 527 PRGKIYEIYLT LHKPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPS PDS 586
 |:|: ||: ||: ||: | :| | : |||: ||: |||| |||||: || || :| :
 Db 560 PQGRVYEMYVTVHRKETMRPPMDDSQTLLTPV VSCGPPGALLTRPVVLTMHHCADPNTED 619

Qy 587 WSLRLKKQSCG SWEDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVAAA 646
 | : || |: | ||||: ||| : | :|: ||: || | :||| : : |||
 Db 620 WKILLKNQAAQGWEDVVVVG EENFTTPCYIKLDAEACHILTENLSTYALVGHSTTKAAA 679

Qy 647 KRLKLLLFAPVACTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYH 706
 ||||| :| |: |: ||||: ||||| || ||||: : ||: ||||: ||: |||| | |
 Db 680 KRLKLAI FGPLCCSSLEYSIRVYCLDDTQDALKEILHLERQTGGQLLEEPKALHFKGSTH 739

Qy 707 NLRLSIHDVPSSLWKSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSD LACKLWV 766
 ||||| |||: ||||| ||||| ||||: ||: ||| ||||| || | :| :| ||| |
 Db 740 NLRLSIHDIAHSLWKSKLLAKYQEIPFYHVWSGSQRNLHCTFTLERFSLNTVELVCKLCV 799

Qy 767 WQVEGDGQSFSINFNITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISSLDPP 826
 ||||: || | :| : : : :| | : : : |||| || ||||: |||| |
 Db 800 RQVEGEGQIFQLNCTVSE EPTGIDLPLLD PANTITTVTGPSAFSIP LPIRQKLCSSLDAP 859

Qy 827 CRRGADWRTLAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQP 886
 || ||| || ||: || |: ||: ||| || |: ||||: ||: |||| ||| : :| :
 Db 860 QTRGHDWRMLAHKLNLD RYLYNFATKSSPTGVILDLEWAQNFPDGNLSMLAAVLEEMGRH 919

Qy 887 DAGLFTVSEAE 897
 : : :| :
 Db 920 ETVVSLAAEGQ 930

RESULT 8

Q8JGT4

ID Q8JGT4 PRELIMINARY; PRT; 943 AA.

AC Q8JGT4;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE UNC-5 receptor.

OS *Xenopus laevis* (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

OC Xenopodinae; *Xenopus*.

OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Anderson R.B., Holt C.E.;
 RT "Expression of UNC-5 in the developing Xenopus visual system."
 RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY099459; AAM34486.1; -.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; tsp_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Immunoglobulin domain; Receptor.
 SQ SEQUENCE 943 AA; 105083 MW; A024E24A7EDB6175 CRC64;

Query Match 55.2%; Score 2646.5; DB 13; Length 943;
 Best Local Similarity 53.0%; Pred. No. 9.3e-235;
 Matches 496; Conservative 163; Mismatches 229; Indels 47; Gaps 8;

Qy	10	ALLGIVLAAWLRG-----SGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKPVL	62
		: : : : : :	
Db	10	AALAAILVALILSCNFPSTAGIEYSDVLPDSFPSAPAESLPHFLLEPEDAYIVKNKPVE	69
Qy	63	LVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQQVEKVFGLLEEY	122
Db	70	LVCKANPATQIYFKCNGEWVNQNDHITKERVDDVTGLVVREVQIEVSRQQVEELFGLLEDY	129
Qy	123	WCQCVAWSSSGTTKSKQAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPGIPPAEVE	182
Db	130	WCQCVAWSSAGTTKSKRSYVRIAYLRKNFDQEPLGKEVALEQEALLQCRPPEGVPPEAVE	189
Qy	183	WLRNEDLVDPISLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAAVIVYVN	242
		: : :	
Db	190	WLKNEEIIDPTKDTNFLTIDHNLIIKQARLSDTANYTCVSKNIVAKRRSTTATVIVFVN	249
Qy	243	GGWSTWTEWSVCSASCGRGWQKRSRSCCTNPAPLNGGAFCEGQNVQKTACATLCPVDGWS	302
		: :	
Db	250	GGWSSWTEWSPCNRRCGHGWQKRTCTNPAPLNGGTMCEGQQYQKFACNTMCPVDGGWT	309
Qy	303	PWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDTNRCTSDLCVHS-----	352
		: : :	

Db 310 EWSKWSACSTECHWRSRECNAPTPKNGGKDCSGMLLDSKNCTDGLCMQNKRVLGETKSR 369

Qy 353 -ASGPEDVALYVGL-IAVAVCLVLLLLVLILVYCRKKEGLSDVDADSS-ILTSGFQPVSI 409
 |||| | | : | : : : | : | | | : | : | | | | : |

Db 370 LLESTGDVALYAGLVVAIFIVIILMAVGIVVYRRNCREFDTDITDSSAALTGGFHPVNF 429

Qy 410 KPSKADNPHELL--TIQPDLSSTTTTYYQGSICPRQDGSPKFKQLTNGHLLSPLGGGRHTLH 467
 | | : | | | : : |||| : | : : | | : | : | | | : : :

Db 430 KTSRHDNSQLIHPAMQPDLTANAGIYRGNMYALQDS-ADKIPMTNSPLLDPLPNLKIKVY 488

Qy 468 HSS-----PTSEAEFEVSRLSTQN-----YFRSLPRGTSNMTYGTG 503
 : || : : : | : : || : ||

Db 489 NSSTVGSSPGIHDGNNLLGKTPTGTYPSDNNIMNARNKNMSMQHLLTLPRDSSNSVTGTG 548

Qy 504 NFLGGRIMIPNTGISLLIPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTLLSPIVSCGP 563
 |||| | ||| : |||| | || : || || : || : | : | | || : |||| : ||||

Db 549 GSLGGRLTFPNTGVSLIPQGAIPQKYYEYMLINKRENTVLPSEGTQTILSPIITCGP 608

Qy 564 PGVLLTRPVILAMDHCGEPSDWSLRLKKQSCGSEWEDVLHLGEEAPSHLYYCQLEASA 623
 | : || : |||| : | | : : | | : || | : || : || : | | : |||| : :

Db 609 TGLLLCKPVILTVPHCADINTSDWILQLKTQSHQGNWEEVVTLINEETLNTPCYCQLESHS 668

Qy 624 CYVFTEQLGRFALVGEALSVAARKLKLFLFAPVACTSLEYNIRVYCLHDTHDALKEVVQ 683
 | : : || : | ||| : | : ||| : |||| : |||| : |||| : |||| : |||| : ||||

Db 669 CHTLLDQLGTYAFVGESYSRSAIKRLQLAIFAPMLCTSLEYNLKVYCVEDTPDALKEVLE 728

Qy 684 LEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSSLWWSKLLVSYQEIPFYHIWNGTQRY 743
 ||| ||| | : || : | |||| |||| : | ||| : ||| : |||| : |||| : ||||

Db 729 LEKTLGGYLVEEPKLLMFKDSYHNLRLSIHDIPHSLWRSKLMAKYQEIPFYHIWSGSQRT 788

Qy 744 LHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINFNITKDTRFAELLALESEAGVPAL 803
 |||| |||| | : : : | || : | |||| : || | : : : : : : : |

Db 789 LHCTFTLERYSLAATELTCKICVRQVEGEGQIFQLHTLLEENVKSFDPFCSQAENSVTTH 848

Qy 804 VGPSAFKIPFLIRQKIISLDPCCRAGADWRTLAQKLHLDHLSFFASKPSPTAMILNLW 863
 : || |||| |||| : || | || || |||| : | : | : || : || : || : ||

Db 849 LGPYAFKIPFSIRQKICNSLDAPNSRGNDWRLLAQKLCMDRYLNYPATKASPTGVILDW 908

Qy 864 EARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAE 898
 || | : | : | : | : : | : : :

Db 909 EALHQDDGDLNTLASALEEMGKSEMMLVMATDGDC 943

RESULT 9

Q80Y85

ID Q80Y85 PRELIMINARY; PRT; 1008 AA.

AC Q80Y85;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Unc5h2 protein (Fragment).

GN UNC5H2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC048162; AAH48162.1; -.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; tsp_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 FT NON_TER 1 1
 SQ SEQUENCE 1008 AA; 110438 MW; BCE5CA0EC537C130 CRC64;

Query Match 54.0%; Score 2585; DB 11; Length 1008;
 Best Local Similarity 53.7%; Pred. No. 4.9e-229;
 Matches 505; Conservative 151; Mismatches 235; Indels 50; Gaps 14;

Qy 1 MAVRPGLWPALLGIVLAAW-----LRG--SGAQQSATVANPVPGANPDLLPHFLVEPEDV 53
| | |: ||| :| | | | | : : | | : ||:|:|:|
Db 75 MRARSGVRSALLLALLLCWDPTPSLAGVDSAGQ---VLPDSYPSAPAEQLPYFLLPEQDA 131

Qy 54 YIVKNKPVLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSROQV 113
||||||| | |:| ||||:||||||| | ||| : | | :|| | |:| |||||
Db 132 YIVKNKPVLELHCRAFPATQIYFKCNGEWVSQNDHVTQESLDEATGLRVREVQIEVSRQOV 191

Qy 114 EKVFGLEEYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPP 173
|:| ||||:||||||| |||||:||||| ||||:||||||| | : :| ||||
Db 192 EELFGLEDYWCQCVAWSSSGTTKSRRAYIRIAYLRKNFDQEPLAKEVPLDHEVLLQCRPP 251

Qy 174 EGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSA 233
||:| |||||:||||:|:| | | :| :|:|:| ||||:||||||| ||||:|
Db 252 EGVPAEVEWLRNEDVIDPAQDTNFLTIDHNLIIRQARLSDTANYTCVAKNIVAKRRST 311

Qy 234 SAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCCTNPAPLNGGAFCEGQNVQKTACAT 293
:| ||||| ||| | | |||||:|:| ||||| ||||| | |||| |
Db 312 TATVIVYVNGGWSSWAEWSPCSNRCGRGWQKRTRTCTNPAPLNGGAFCEGQAFQKTACTT 371

Qy 294 LCPVDGWSWPWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDRNCTSDLCVHSA 353
:||||:|: | ||||| :| ||||| | |:| | :| || |:| | | :
Db 372 VCPVDGAWTEWSKWSACSTECAHWSRECMAPPQNGGRDCSGTLLDSKNCTDGLCVLTL 431

Qy 354 SGPEDVALYVGL-IAVAVCLVLLLVLILVYCRKKEGLSDVDADSS-ILTSGFQPVSIKP 411
|||| | | :| | : :| | :|| | | :|: | | | | | | :|
Db 432 ETSGDVALYAGLVAVFVVVAVLMAVGIVYRRNCRDFDTDITDSSAALTGGFHPVNFKT 491

Qy 412 SKADNPHLL--TIQPDLSSTTTTYQGSCLPRQDGPSPKFQLTNGHLLSPLGGGRHTLHHS 469
: : || | | : ||| : : |:| : | | : | :|| | | | : : :|
Db 492 ARPNNPQLLHPSAPPDLTASAGIYRGPVYALQDS-ADKIPMTNSPLDPLPSLKIKVYNS 550

Qy 470 S-----PTSEAEFVSRLSTQNYFRS-----LPRGTSNMTY 500
| | : : | | : : || | | :
Db 551 STIGSGSGLADGADLLGVLPPTYPGDF-SRDTHFLHLSASLGSHLLGLPRDPSSSVS 609

Qy 501 GTFNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYTLHKPEDVRLPLA-GCQTLLSPIV 559
||| | ||| :| ||:|:| | ||:| | :|| :| | | | | | :|
Db 610 GTFGCLGGRLSLPGTGVSLVPNGAIPQKIFYDLYLHINKAEST-LPLSEGSQTVLSPSV 668

Qy 560 SCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEGSWEDVLHLGEEAPSHLYYCQL 619
:|| | |:| |||:| : | | | :|| |: :| ||:|: | || : ||||
Db 669 TCGPTGLLLCRPVLTVPHCAEVIAGDWIFQLKTQAHQGHWEVVTLDEETLNTPCYCQL 728

Qy 620 EASACYVFTEQLGRFALVGEALSVAALKRLKLLLFAPVACTSLEYNIRVYCLHDTHDALK 679
|| :||: :||| : :||: | :| |||:| :||| |||||:| |||| | ||
Db 729 EAKSCHILLDQLGTYVFMGESYSRSAVKRLQLAIFAPALCTSLEYSRLVYCLEDTPVALK 788

Qy 680 EVVQLEKQLGGQLIQEPRVLHFKDSYHNLRSLIHDVPSSLWKSLLVSYQEIPFYHIWNG 739
|:|:|:| | | |:|:| | | ||||| ||||:| | :|:| | |||||:| |
Db 789 EVLELERTLGGYLVEEPKPLLFKDSYHNLRSLHDIPHAHWSKLLAKYQEIPFYHVWNG 848

Qy 740 TQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINFNITKDTRFAELLALESEAG 799
:| | ||||| | : : : ||: | |||:| | | : : | | | | |
Db 849 SQRALHCTFTLERHSLASTEFTCKVCVRQVEGEGQIFQLHTTLA-ETPAGSLDALCSAPG 907

Qy 800 --VPALVGPSAFKIPFLIRQKIISSLDPPCRRGADWRTLAQKLHLDShLSFFASKPSPTA 857

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      :  :|| |||| | ||| | || | || ||| :| :||:|:| |||
Db      908 NAITTQLGPYAFKIPLSIRQKICSSLDAPNSRGNDWRLLAQKLSMDRYLNYFATKASPTG 967

Qy      858 MILNLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAEC 898
      :||:|||| | |:|: ||:|: |:| : : : :|
Db      968 VILDLWEARQQDDGDLNSLASALEEMGKSEMLVAMATDGDC 1008

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RESULT 10

Q8K1S3

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ID      Q8K1S3      PRELIMINARY;      PRT;      945 AA.
AC      Q8K1S3;
DT      01-OCT-2002 (TrEMBLrel. 22, Created)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Netrin receptor Unc5h2.
GN      UNC5H2.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Engelkamp D.;
RT      "Cloning of three mouse unc-5 genes and their expression patterns at
RT      mid-gestation.";
RL      Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AJ487853; CAD32251.1; -.
DR      MGD; MGI:894703; Unc5h2.
DR      GO; GO:0004872; F:receptor activity; IEA.
DR      GO; GO:0007165; P:signal transduction; IEA.
DR      InterPro; IPR000488; Death.
DR      InterPro; IPR003599; Ig.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003598; Ig_c2.
DR      InterPro; IPR000884; TSP1.
DR      InterPro; IPR008085; TSP_1.
DR      InterPro; IPR000906; ZU5.
DR      Pfam; PF00531; death; 1.
DR      Pfam; PF00047; ig; 1.
DR      Pfam; PF00090; tsp_1; 2.
DR      Pfam; PF00791; ZU5; 1.
DR      PRINTS; PR01705; TSP1REPEAT.
DR      SMART; SM00005; DEATH; 1.
DR      SMART; SM00409; IG; 2.
DR      SMART; SM00408; IGc2; 1.
DR      SMART; SM00209; TSP1; 2.
DR      SMART; SM00218; ZU5; 1.
DR      PROSITE; PS50017; DEATH_DOMAIN; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
DR      PROSITE; PS50092; TSP1; 2.
KW      Immunoglobulin domain; Receptor.
SQ      SEQUENCE      945 AA; 103738 MW; 80E896F0F0E06012 CRC64;

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Query Match          53.8%; Score 2578.5; DB 11; Length 945;
Best Local Similarity 53.2%; Pred. No. 1.8e-228;
Matches 506; Conservative 150; Mismatches 235; Indels 61; Gaps 15;

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Qy 1 MAVRPGLWPALLGIVLAAW-----LRG--SGAQQSATVANPVPGANPDLLPHFLVEPEDV 53
| | |: ||| :| | | | | : : | | : ||:|:|:|

Db 1 MRARSGVRSALLLALLLCWDPTPSLAGVDSAGQ---VLPDSYPSAPAEQLPYFLLPEQDA 57

Qy 54 YIVKNKPVLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQV 113
||||||| | |:| ||||:||||||| | ||| : | | :|| | |:| |||||

Db 58 YIVKNKPVELHCRAFPATQIYFKCNGEWVSQNDHVTQESLDEATGLRVREVQIEVSRQV 117

Qy 114 EKVFGLLEEYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPP 173
|:| ||||:||||||| |||||:||||||| |||||:||||||| |: :| |||

Db 118 EELFGLEDYWCQCVAWSSSGTTKSRRAYIRIAYLRKNFDQEPLAKEVPLDHEVLLQCRPP 177

Qy 174 EGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSA 233
||:| |||||:||||:| | | :| :|:|:| |||||:||||||| |||||:|

Db 178 EGVPAEVEWLKNEDVIDPAQDTNFLTIDHNLIRQARLSDTANYTCVAKNIVAKRRST 237

Qy 234 SAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCNPNAPLNGGAFCEGQNVQKTACAT 293
:| ||||| ||||:| ||| || |||||:|:||||||| ||||| |

Db 238 TATVIVYVNGGWSSWAEWSPCSNRCGRGWQKRTRTCTNPAPLNGGAFCEGQAFQKTACTT 297

Qy 294 LCPVDGSWSPWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDRNCTSDLCV--- 350
:||||:|: ||||| :| ||||| | |:||| :| || |:| ||| |||

Db 298 VCPVDGAWTEWSKWSACSTECAHWSRECMAPPPQNGGRDCSGTLLDSKNCTDGLCVLNQ 357

Qy 351 -----HSASGPEDVALYVGL-IAVAVCLVLLLLVLILVYCRKKEGLDSDVADSS-IL 400
| | |||| || |:| | : :| | :|| | |:| || |

Db 358 RTLNDPKSHPLETSGDVALYAGLVVAVFVVAVLMAVGIVYRRNCRDFDTDITDSSAAL 417

Qy 401 TSGFQPVSIKPSKADNPHELL--TIQPDLSSTTTTYQGSICPRQDGPSPKFQLTNGHLLSP 458
| || ||: | :| :|| || : |||: : |:| : || :| :|| |||

Db 418 TGGFHPVNFKTARPNNPQLLHPSAPPDLTASAGIYRGPVYALQDS-ADKIPMTNSPLLD 476

Qy 459 LGGGRHTLHHSS-----PTSEAEFVSRLSTQNYFRS----- 490
| : :|| | : :| || : :|

Db 477 LPSLKIKVYNSSTIGSGSLADGADLLGVLPPGTYPGDF-SRDTHFLHLRSASLGSQHLL 535

Qy 491 -LPRGTSNMTYGTFNFLGGRIMIPNTGISLLIPDAIPRGKIYEIYTLHKPEDVRLPLA 549
||| |: || |||| :| ||:|:| |||:| |:| |:| :| |||

Db 536 GLPRDPSSSVSGTFGCLGGRLSLPGTGVSLVPNGAIPQGKFYDLYLHINKAEST-LPLS 594

Qy 550 -GCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEGSWEDVLHLGE 608
| ||:| | |:| | |:| |||:| : || | :|| |:| |:| |:| :|

Db 595 EGSQTVLSPSVTCGPTGLLLCRPVVLTVPHCAEVIAGDWIFQLKTQAHQGHWEVVTLDE 654

Qy 609 EAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVA AAKRLKLLLFAPVACTSLEYNIRV 668
| : ||||| :|| :||| : :||| | :| |||:| :|| | ||||:|

Db 655 ETLNTPCYCQLEAKSCHILLDQLGTYVFMGESYSRSASVAKRLQLAIFAPALCTSLEYSLRV 714

Qy 669 YCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSSLWKSLLVSY 728
||| || ||||:|:| || |:|:| | |||||:|:| |:| |:| |

Db 715 YCLEDTPVALKEVLELERTLGGYLVEEPKPLLFKDSYHNLRLSLHDIPHAWRSKLLAKY 774

Qy 729 QEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINFNITKDTRF 788
|||||:|:| ||||| | :|| |:| ||||:| |:| : :|

Db 775 QEIPFYHVWNGSQRALHCTFTLERHSLASTEFTCKVCVRQVEGEGQIFQLHTTLA-ETPA 833

Qy 789 AELLALESEAG--VPALVGPSAFKIPFLIRQKISSLDPPCRGGADWRTIAQKLHLDL 846
 | | | | | : : | | | | | | | | | | | : | : |
 Db 834 GSLDALCSAPGNAITTLQGPYAFKIPLSIRQKICSSLDAPNSRGNDWRLLAQKLSDRYL 893
 Qy 847 SFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAEC 898
 : : | : | | : | : | | | : : | : : : : : : : |
 Db 894 NYFATKASPTGVILDLWEARQQDDGLNSLASALEEMGKSEMLVAMATDGDC 945

RESULT 11

008722

ID 008722 PRELIMINARY; PRT; 945 AA.
 AC 008722;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Transmembrane receptor UNC5H2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97271897; PubMed=9126742;
 RA Leonardo E.D., Hinck L., Masu M., Keino-Masu K., Ackerman S.L.,
 RA Tessier-Lavigne M.;
 RT "Vertebrate homologues of C. elegans UNC-5 are candidate netrin
 RT receptors.";
 RL Nature 386:833-838(1997).
 DR EMBL; U87306; AAB57679.1; -.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; tsp_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Immunoglobulin domain; Receptor.
 SQ SEQUENCE 945 AA; 103520 MW; 6E9C2A262E560B9B CRC64;

Query Match 53.8%; Score 2578.5; DB 11; Length 945;
 Best Local Similarity 53.0%; Pred. No. 1.8e-228;
 Matches 509; Conservative 142; Mismatches 231; Indels 79; Gaps 17;

Qy 1 MAVRPGLWPALLGIVLAAW-----LRG--SGAQQSATVANPVPGANPDLLPHFLVEPEDV 53
| | | ||| :| | | || | : : | | : ||||:||||
Db 1 MRARSGARGALLLALLLCWDPTPSLAGIDSGGQ---ALPDSFPSAPAEQLPHFLLPEDEA 57

Qy 54 YIVKNKPVLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQV 113
||||||| | |:| ||||:||||||| | || : | | :|| | |:| |||||
Db 58 YIVKNKPVLELHCRAFPATQIYFKCNGEWVSQKGHVTQESLDEATGLRIREVQIEVSRQV 117

Qy 114 EKVFGLLEEYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPP 173
|::|||:||||||| |||||:||||| ||||:||||||| | : :| |||
Db 118 EELFGLLEDYWCQCVAWSSSGTTKSRRAYIRIAYLRKNFDQEPLAKEVPLDHEVLLQCRPP 177

Qy 174 EGIPPAEVEWLRNEDLVDPSPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSA 233
||:| ||||:||||:|:| | | :| :|:|:||||:||||||| ||||:|
Db 178 EGVPAEVEWLRNEDVIDPAQDTNFLTIDHNLIRQARLSDTANYTCVAKNIVAKRRST 237

Qy 234 SAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCNPNAPLNGGAFCEGQNVQKTACAT 293
:| ||||| |||:| ||| || |||||:|:||||||| ||||| |
Db 238 TATVIVYVNGGWSSWAEWSPCSNRCGRGWQKRTRTCTNPAPLNGGAFCEGQACQKTACTT 297

Qy 294 LCPVDGSWSPWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDRNCTSDLCV--- 350
:||||:|: ||||| :| ||||| | |:| | :| || |:| | ||
Db 298 VCPVDGAWEWSKWSACSTECAHWSRECMAPPPQNGGRDCSGTLLDSKNCTDGLCVLNQ 357

Qy 351 HSASGPE-----DVALYVGL-IAVAVCLVLLLLVLILVYCRKKEGLDSDVADSS-IL 400
: : | : |||| || :|| | | :| : | :|| | | :|: || |
Db 358 RTLNDPKSRPLEPSGDVALYAGLVAVFVVLAVLMAVGIVYRRNCRDFDTDITDSSAAL 417

Qy 401 TSGFQPVSIKPSKADNPHELL--TIQPDLSSTTTTYQGSCLPRQDGPSPKFQLTNGHLLSP 458
| || ||: | :| || | : |||: : | :| : || : | :|| || |
Db 418 TGGFHPVNFKTARPSNPQLHPSAPPDLTASAGIYRGPVYALQDS-ADKIPMTNSPLLD 476

Qy 459 L-----GGG-----RHTLHSSPTSEAEFVS 480
| | | | | | | | | :
Db 477 LPCLKIKVYDSSTIGSGAGLADGADLLGLVPPGTYPGDFSRDTHFLHLRS-----A 527

Qy 481 RLSTQNYFRSLPRGTSNMTYGTNFNLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLT LHK 540
| :| : ||| | : ||| |||| || ||:|:| | ||:| | :|| || |
Db 528 SLGSQ-HLLGLPRDPSSSVSGTFGCLGGRLTIPGTGVSLVPNGAIPQGKFYDLYLRINK 586

Qy 541 PEDVRLPLA-GCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEGS 599
| ||:| | |:| | |:| | |:| | : || | | :|| | :|
Db 587 TEST-LPLSEGSQTVLSPSVTCGPTGLLLCRPVVLTVPHCAEVIAGDWIFQLKTQAHQGH 645

Qy 600 WEDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVAALKRLKLLLFAPVAC 659
||:| | || : ||||| |:|: :||| : ||: | :| ||:| :|| |
Db 646 WEEVVTLDDETLNTPCYCQLEAKSCHILLDQLGTYVFTGESYSRSAVKRLQLAIFAPALC 705

Qy 660 TSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNRLSLHDVPSSL 719
||||:|||| | ||||:|:| || |:|:| | ||||| |:| :
Db 706 TSLEYSRLVYCLEDTPAALKEVLELERTLGGYLVEEPKTL LFKDSYHNRLSLHDIPHAAH 765

Qy 720 WSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSIN 779
|:| || ||||| |:|:| ||||| | :|:| ||:| | ||:| | :|
Db 766 WRSKLLAKYQEIPFYHVWNGSQKALHCTFTLERHSLASTEFTCKVCVRQVEGEGQIFQLH 825

Qy 780 FNITKDTRFAELLALESEAGVPAL--VGPSAFKIPFLIRQKIISSLDPPCRRGADWRTLA 837


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      ||| |: ||| |||| :| ||:||||| |||:| |::|| ::| | |||:
Db      536 GLPRDPSSSVSGTFGCLGGRLSLPGTGVSLLPNGAIPQGKFYDLYLHINKAEST-LPLS 594

Qy      550 -GCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDWSLRLKKQSCEGSWEDVLHLGE 608
      | ||:|||| |:||| ||:| |||:| : || | | :|| |: :| ||:|: | |
Db      595 EGSQTVLSPSVTCGPTGLLLCRPVVLTVPHCAEVIAGDWIFQLKTQAHQGHWEVVTLDE 654

Qy      609 EAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVAALKRLKLLLFAPVACTSLEYNIRV 668
      | : ||||| :||: :||| : :||: | :| |||:| :||| |||||:| |
Db      655 ETLNTPCYCQLEAKSCHILLDQLGSYVFMGESYSRSAVKRLQLAIFAPALCTSLEYSLRV 714

Qy      669 YCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSLIHDVPSSLWKSLLVSY 728
      ||| || |||||:| |: ||| |:| |: | ||||| |||||:| |: | |:| ||| |
Db      715 YCLEDTPVALKEVLELERTLGGYLVEEPKPLLFKDSYHNLRLSLHDIPAHWRSKLLAKY 774

Qy      729 QEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINFNITKDRF 788
      |||||:| |:| | ||||| | ::: ||: | |||:| | : : : |
Db      775 QEIPFYHVWNGSQRALHCTFTLERHSLASTEFTCKVCVRQVEGEGQIFQLHTTLA-ETPA 833

Qy      789 AELLALESEAG--VPALVGPSAFKIPFLIRQKIISSLDPPCRRGADWRTLAQKLHLDShL 846
      | || | | : :|| |||| |||| |||| | || ||| ||||| :| :|
Db      834 GSLDALCSAPGNAITTQLGPYAFKIPLSIRQKICSSLDAPDSRGNDWRLLAQKLSMDRYL 893

Qy      847 SFFASKPSPPTAMILNLWEARHFNGNLSQLAAAVAGLGQPDAGLFTVSEAEC 898
      ::||:| ||| :||:|||| | |:| :||:| :|: : : : : :|
Db      894 NYFATKASPTGVILDLWEARQQDDGDLNSLASALEEMGKSEMLVAMATDGDC 945

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RESULT 13

Q8IZJ1

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ID   Q8IZJ1          PRELIMINARY;          PRT;    934 AA.
AC   Q8IZJ1;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Transmembrane receptor UNC5H2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22246081; PubMed=12359238;
RA   Komatsuzaki K., Dalvin S., Kinane T.B.;
RT   "Modulation of G(alpha(2)) signaling by the axonal guidance molecule
RT   UNC5H2.";
RL   Biochem. Biophys. Res. Commun. 297:898-905(2002).
DR   EMBL; AY126437; AAM95701.1; -.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000884; TSP1.
DR   InterPro; IPR008085; TSP_1.
DR   InterPro; IPR000906; ZU5.

```

DR Pfam; PF00531; death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; tsp_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Receptor.
 SQ SEQUENCE 934 AA; 102433 MW; 225B3F506D52B780 CRC64;

Query Match 53.6%; Score 2566; DB 4; Length 934;
 Best Local Similarity 53.1%; Pred. No. 2.5e-227;
 Matches 498; Conservative 147; Mismatches 250; Indels 42; Gaps 13;

Qy 1 MAVRPGLWPALLGIVLAAW---LRGSGAQQ-SATVANPVPGANPDLLPHFLVEPEDVYIV 56
 | | | | | : | | : | | : | | : | | | | |
 Db 1 MGARSGARGALLLALLLCWDPRLSQAGTDSGSEVLPSDFPSAPAEPLPYFLQEPQDAYIV 60

Qy 57 KNKPVLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQQVEKV 116
 | | | | | | : | | | | | : | | | | | | | | | | : | : | | | | | : | :
 Db 61 KNKPVELRCRAFPATQIFYKCNGEWVSQNDHVTQEGLEATGLRVREVQIEVSRQQVEEL 120

Qy 117 FGLEEYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPEGI 176
 | | | : | | | | | | | : | | | : | | | | | | | | | | | : | : | | | | :
 Db 121 FGLEDYWCQCVAWSSAGTTKSRRAYVRIAYLRKNFDQEPLGKEVPLDHEVLLQCRPPEGV 180

Qy 177 PPAEVEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAA 236
 | | | | | : | | : | | : | : | : | | | : | | | | | | | | | | : | : |
 Db 181 PVAEVEWLKNEVDIDPTQDTNFLTIDHNLIIQRARLSDTANYTCVAKNIVAKRRSTTAT 240

Qy 237 VIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCCTNPAPLNGGAFCEGQNVQKTACATLCP 296
 | | | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | : | : |
 Db 241 VIVYVNGGWSSWAEWSPCSNRCGRGWQKRTCTNPAPLNGGAFCEGQAFQKTACTTICP 300

Qy 297 VDGSWSPWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDTNRCTSDLCVHSASGP 356
 | | : | : | | | | | : | | | | | | | : | | | : | | | | : | | | : | :
 Db 301 VDGAWTEWSKWSACSTECAHWSRECMAPPQNGGRDCSGTLLDSKNCTDGLCMQMLEAS 360

Qy 357 EDVALYVGL-IAVAVCIVLVLLLVILVYCRKKEGLSDSDVADSS-ILTSGFQPVSIKPSKA 414
 | | | | | : | : | : | : | : | | | : | : | | | | | | | : | :
 Db 361 GDAALYAGLVVAIFVVVAIIMAVGVVVYRRNCRDFDITDSSAALTGGFHPVNFKTARP 420

Qy 415 DNPHELL--TIQPDLSSTTTTYQGSCLCPQDGPSPKFQLTNGHLLSPLGGGRHTLHHSSTP 472
 | | | : : | | : | : | : | : | | : | | : | | : : | | |
 Db 421 SNPQLLHPSVPPDLTASAGIYRGFVYALQDS-TDKIPMTNSPLLDPLPSLKVKVYSSSTT 479

Qy 473 -----SEAEFVSRLSTQNY-----FRS-----LPRGTSNMTYGTFN 504
 : : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 480 GSGPGLADGADLLPGTYPSPDFARDTHFLHLSASLGSQQLLGLPRDPGSSVSGTGF 539

Qy 505 FLGGRLMIPNTGISLLIPPDAPRGKIYEIYLT LHKPEDVRLPLA-GCQTLLSPIVSCGP 563
 | | | | | | | : | | : | | : | | : | : | | | | | : | | : | | | | |

DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; tsp_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Receptor.
 SQ SEQUENCE 945 AA; 103637 MW; 56064E335F323447 CRC64;

Query Match 53.4%; Score 2558.5; DB 4; Length 945;
 Best Local Similarity 52.7%; Pred. No. 1.3e-226;
 Matches 501; Conservative 148; Mismatches 244; Indels 57; Gaps 15;

Qy	1	MAVRPGLWPALLGIVLAAW---LRGSGAQQ-SATVANPVPGANPDLLPHFLVEPEDVYIV	56
		: : : : : :	
Db	1	MGARSGARGALLLALLLCWDPRLSQAGTDSGSEVLPSDFPSAPAEPLPYFLQEPQDAYIV	60
Qy	57	KNKPVLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRQQVEKV	116
		: : : : : ::	
Db	61	KNKVELRCRAFPATQIFYKCNGEWVSQNDHVTQEGLDEATGLRVREVQIEVSRQQVEEL	120
Qy	117	FGLEEYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPEGI	176
		: : : : : : :	
Db	121	FGLEDYWCQCVAWSSAGTTKSRRAYVRIAYLRKNFDQEPLGKEVPLDHEVLLQCRPPEGV	180
Qy	177	PPAEVEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAA	236
		: : : : : : : :	
Db	181	PVAEVEWLKNEDVIDPTQDTNFLTIDHNLIRQARLSDTANYTCVAKNIVAKRRSTTAT	240
Qy	237	VIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCCTNPAPLNGGAFCEGQNVQKTACATLCP	296
		: : : :	
Db	241	VIVYVNGGWSSWAEWSPCSNRCGRGWQKRTCTNPAPLNGGAFCEGQAFQKTACTTICP	300
Qy	297	VDGSWSPWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDTNRCTSDLCVHS----	352
		: : : : : : : :	
Db	301	VDGAWTEWSKWSACSTECAHWSRECMAPPPQNGGRDCSGTLLDSKNCTDGLCMQNKKTL	360
Qy	353	-----ASGPEDVALYVGL-IAVAVCLVLLLLVLILVYCRKKEGLDSDVADSS-ILT	401
		: : : : :	
Db	361	SDPNSHLLEASG--DAALYAGLVVAIFVVVAILMAVGVVVYRRNCRDFDTDITDSSAALT	418
Qy	402	SGFQPVSIKPSKADNPHELL--TIQPDLTSTTTTYQGSCLPRQDGPSPKFQLTNGHLLSPL	459
		: : : : : : : : : :	
Db	419	GGFHPVNFKTARPSNPQLLHPSVPPDLTASAGIYRGVPVYALQDS-TDKIPMTNSPLLDPL	477
Qy	460	GGRHTLHHSSPT-----SEAEFVSRLSTQNY-----FRS-----L	491
		: : : : :	
Db	478	PSLKVKVYSSSTTGSGPGLADGADLLGVLPPTGTPSDFARDTHFLHLRSASLGSQQLLGL	537
Qy	492	PRGTSNMTYGTFFNLGGRLMIPNTGISLLIPPDAIPRGIYEIYLTLHKPEDVRLPLA-G	550
		: : : : : : :	
Db	538	PRDPGSSVSGTFGCLGGRLSIPGTGVSLVPNGAIPQGKFYEMYLLINKAEST-LPLSEG	596

QY 551 CQTLSPIVSCGPPGVLLTRPVILAMDHCGEPPSDSWSLRLKKQSCGSWEDVLHLGEEA 610
 Db 597 TQTVLSPSVTCGPTGLLLCRPVILTMPHCAEVSARDWIFQLKTQAHQGHWEVVTLDEET 656

QY 611 PSHLYYCQLEASACYVFTEQLGRFALVGEALSVAALKRLKLLLFAPVACTSLEYNIRVYC 670
 Db 657 LNTPCYCQLEPRACHILLDQLGTYVFTGESYSRSAVKRLQLAVFAPALCTSLEYSRLVYC 716

QY 671 LHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSSLWKSLLVSYQE 730
 Db 717 LEDTPVALKEVLELERTLGGYLVEEPKPLMFKDSYHNLRLSLHDLPHAHWRSKLLAKYQE 776

QY 731 IPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINFNITKDTRFAE 790
 Db 777 IPFYHIWSGSQKALHCTFTLERHSLASTEITCKICVRQVEGEGQIFQLHTTLA-ETPAGS 835

QY 791 LLALESEAG--VPALVGPSAFKIPFLIRQKIISLDPPCRAGDWRTLAQKLHLDShLSF 848
 Db 836 LDTLCSAPGSTVTTQLGPYAFKIPLSIRQKICNSLDAPNSRGNDWRMLAQKLSMDRYLNY 895

QY 849 FASKPSPTAMILNLWEARHFNGNLSQLAAAVAGLGQPDAGLFTVSEAEC 898
 Db 896 FATKASPTGVILDLWEALQQDDGDLNSLASALEEMGKSEMLVAVATDGDC 945

RESULT 15

Q8K1S2

ID Q8K1S2 PRELIMINARY; PRT; 956 AA.
 AC Q8K1S2;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Netrin receptor Unc5h4.
 GN UNC5H4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Engelkamp D.;
 RT "Cloning of three mouse unc-5 genes and their expression patterns at
 RT mid-gestation.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ487854; CAD32252.1; -.
 DR MGD; MGI:2389364; Unc5h4.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000215; Serpin.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.

DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; tsp_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Immunoglobulin domain; Receptor.
 SQ SEQUENCE 956 AA; 106351 MW; DFDF07839C10C68D CRC64;

Query Match 45.9%; Score 2200; DB 11; Length 956;
 Best Local Similarity 45.5%; Pred. No. 1.6e-193;
 Matches 431; Conservative 159; Mismatches 280; Indels 78; Gaps 15;

Qy 8 WPALLGIVLAAWLGRS----GAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKPVLL 63
 | | : | : | : : | | | | : | | | : | : |
 Db 15 WLPWLGLFF--WAAGAAAARGADGSEILPDSIPSA-PGTLPHFIEEPEDAYIIKSNPIAL 71

 Qy 64 VCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSROQVEKVFGLLEEW 123
 | | | | | | | | | | : | | | | | | | | : | : |
 Db 72 RCKARPAMQIFFKCNGEVHQNEHVSEESLDESSGLKVREVFINVTRQQVEDFHGPEDYW 131

 Qy 124 CQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPGIPPAEVEW 183
 | | | | | | : | : | : | : | | | | : | : | : | | | | |
 Db 132 CQCVAWSHLGTSKSRKASVRIAYLRKNFEQDPQGREVPIEGMIVLHCRPPEGVPAAEVEW 191

 Qy 184 LRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAAVIVYVNG 243
 | : | : : | | : : : | : | : | : | : | : | : | : | : |
 Db 192 LKNEEPIDSEQDENIDTRADHNLIRQARLSDSGNYTCMAANIVAKRRSLSATVVVYVNG 251

 Qy 244 GWSTWTEWSVCSASCGRGWQKRSRSTCTNPAPLNGGAFCEGQNVQKTACATLCPVDGWSWP 303
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 252 GWSSWTEWSACNVRCGRGWQKRSRTCTNPAPLNGGAFCEGMSVQKITCTALCPVDGSWEV 311

 Qy 304 WSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDRNCTSDLCV----- 350
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 312 WSEWSVCSPECEHLRIRECTAPPPRNGGKFCEGLSQESENCTDGLCILDKKPLHEIKPQR 371

 Qy 351 ---HSASGPEDVALYVGLIYAVVCLVLLLLVLILVYCRKKEGLDSDVADSSILTSGFQPV 407
 | : | | | | | | : | : : : : | | | | | | | | | |
 Db 372 WSRRGIENASDIALYSGL-GAAVVAVAVLVIGVTLYRRSHSDYGVDDVIDSSALTGGFQTF 430

 Qy 408 SIKPSKADNPHLL--TIQPDLSSTTTTYQGSCLPRQDGPSPKFQLTNGHLLSPLG----- 460
 : | : | | : | | : | | : | | | : | : | : | : | : |
 Db 431 NFKTVRQGNLLLLNPAMQPD-LTVSRTYSGPIC-LQD-PLDKELMTESSLFNPLSDIKVK 487

 Qy 461 -----GGRH-----TLHHSSPTSEAEFVSRLSTQNYFR 489
 | | | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 488 VQSSFMVSLGVSEAEYHGKNHSGTFPHGNNRGFSTIHPRNKT----PYIQNLS----- 537

Qy	490	SLPRGTSNMTYGTFTNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLT LHKPEDVRLPLA	549
Db	538	SLPTRTELRTTGVFGHLGGRLVMPNTGVSLLI PHGAI PEENSWEIYMSINQGEP-SLQSD	596
Qy	550	GCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDWSLRLKKQSCEGSWEDVLHLGEE	609
Db	597	GSEVLLSPEVTCGPPDMLVTTTPFALTIPHCADVSEHWNHILKKRTQQGKWEEVMSVEDE	656
Qy	610	APSHLYYCQLEASACYVFTEQLGRFALVGEALSVA AAKRLKLLLFAPVACTSLEYNIRVY	669
Db	657	STS--CYCLDPFACHVLLDSFGTYALTGEPITDCAVKQLKVAVFGCMSCNSLDYNLRVY	714
Qy	670	CLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSSLWKS KLLVSYQ	729
Db	715	CVDNTPCAFAQEVISDERHQGGQLLEEPKLLHFKGNTFSLQVSVLDIP PFLWRIKPFTACQ	774
Qy	730	EIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINFNITKDTRFA	789
Db	775	EVPFSRVWSSNRQPLHCAFSLERYTPTTTTQLSCKICIRQLKGHEQILQVQTSILESERET	834
Qy	790	ELLALESEAGVPALVGPSAFKIPFLIRQKIISSLDPPCRRGADWRTL AQLHLDSHLSFF	849
Db	835	ITFFAQEDSTFPAQTGPKAFKIPYSIRQRICATFDT PNAKGKDWQMLAQKNSINRNLSYF	894
Qy	850	ASKPSPTAMILNLWEARHPFNGNLSQLAAAVAGLGQPDAGLFTVSEAE	897
Db	895	ATQSSPSAVIILNLWEARHQQDGDLSLACALEEIGRTHTKLSNITEPQ	942

Search completed: July 6, 2004, 14:34:59
Job time : 53 secs

OM protein - protein search, using sw model

Run on: July 6, 2004, 14:20:26 ; Search time 17 Seconds
(without alignments)
2750.529 Million cell updates/sec

Title: US-10-624-932-2
Perfect score: 4791
Sequence: 1 MAVRPGLWPALLGIVLAAWL.....AVAGLGQPDAGLFTVSEAE 898

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	298.5	6.2	1584	1	BAI1_HUMAN	O14514 homo sapien
2	296.5	6.2	1172	1	TSP2_HUMAN	P35442 homo sapien
3	293	6.1	1074	1	SM5A_HUMAN	Q13591 homo sapien
4	293	6.1	1172	1	TSP2_MOUSE	Q03350 mus musculu
5	291.5	6.1	1170	1	TSP2_BOVIN	Q95116 bos taurus
6	291	6.1	1077	1	SM5A_MOUSE	Q62217 mus musculu
7	290	6.1	1173	1	TSP1_XENLA	P35448 xenopus lae
8	276	5.8	1093	1	SM5B_HUMAN	Q9p283 homo sapien
9	275.5	5.8	1093	1	SM5B_MOUSE	Q60519 mus musculu
10	275	5.7	1522	1	BAI3_HUMAN	O60242 homo sapien
11	274.5	5.7	1572	1	BAI2_HUMAN	O60241 homo sapien
12	270.5	5.6	1170	1	TSP1_MOUSE	P35441 mus musculu
13	268.5	5.6	1170	1	TSP1_HUMAN	P07996 homo sapien
14	265.5	5.5	1170	1	TSP1_BOVIN	Q28178 bos taurus
15	263	5.5	1178	1	TSP2_CHICK	P35440 gallus gall
16	243	5.1	469	1	PROP_HUMAN	P27918 homo sapien
17	240	5.0	470	1	PROP_CAVPO	Q64181 cavia porce

18	229	4.8	437	1	PROP_MOUSE	P11680	mus musculus
19	201	4.2	867	1	SSPO_BOVIN	P98167	bos taurus
20	199	4.2	1266	1	NGCA_CHICK	Q03696	gallus gall
21	181	3.8	1736	1	ZO1_HUMAN	Q07157	homo sapien
22	178	3.7	1745	1	ZO1_MOUSE	P39447	mus musculus
23	177	3.7	587	1	CO8B_ONCMY	Q90x85	oncorhynchu
24	175.5	3.7	905	1	ATS8_MOUSE	P57110	mus musculus
25	173.5	3.6	630	1	ATS4_RAT	Q9esp7	rattus norv
26	172.5	3.6	1223	1	AT14_HUMAN	Q8wxs8	homo sapien
27	172	3.6	837	1	ATS4_HUMAN	O75173	homo sapien
28	170.5	3.6	1077	1	AT10_HUMAN	Q9h324	homo sapien
29	170.5	3.6	1224	1	AT16_HUMAN	Q8te57	homo sapien
30	169.5	3.5	890	1	ATS8_HUMAN	Q9up79	homo sapien
31	169.5	3.5	934	1	CO6_HUMAN	P13671	homo sapien
32	168	3.5	860	1	ATS6_HUMAN	Q9ukp5	homo sapien
33	168	3.5	1095	1	AT17_HUMAN	Q8te56	homo sapien
34	165.5	3.5	1205	1	ATS3_HUMAN	O15072	homo sapien
35	161.5	3.4	1906	1	AT20_MOUSE	P59511	mus musculus
36	160	3.3	930	1	ATS5_HUMAN	Q9una0	homo sapien
37	160	3.3	930	1	ATS5_MOUSE	Q9r001	mus musculus
38	159.5	3.3	967	1	ATS1_RAT	Q9wuq1	rattus norv
39	159.5	3.3	968	1	ATS1_MOUSE	P97857	mus musculus
40	158.5	3.3	997	1	ATS7_HUMAN	Q9ukp4	homo sapien
41	157	3.3	967	1	ATS1_HUMAN	Q9uhi8	homo sapien
42	156.5	3.3	562	1	AT15_MOUSE	P59384	mus musculus
43	156.5	3.3	807	1	FSPO_RAT	P35446	rattus norv
44	155.5	3.2	1911	1	AT20_HUMAN	P59510	homo sapien
45	155	3.2	584	1	CO8A_HUMAN	P07357	homo sapien

ALIGNMENTS

RESULT 1

BAIL_HUMAN

ID BAIL_HUMAN STANDARD; PRT; 1584 AA.

AC O14514;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Brain-specific angiogenesis inhibitor 1 precursor.

GN BAIL.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Fetal brain;

RX MEDLINE=98054121; PubMed=9393972;

RA Nishimori H., Shiratsuchi T., Urano T., Kimura Y., Kiyono K.,

RA Tatsumi K., Yoshida S., Ono M., Kuwano M., Nakamura Y., Tokino T.;

RT "A novel brain-specific p53-target gene, BAIL, containing

RT thrombospondin type 1 repeats inhibits experimental angiogenesis.";

RL Oncogene 15:2145-2150(1997).

RN [2]

RP INTERACTION WITH BAP1.

RX MEDLINE=98321173; PubMed=9647739;
 RA Shiratsuchi T., Futamura M., Oda K., Nishimori H., Nakamura Y.,
 RA Tokino T.;
 RT "Cloning and characterization of BAI-associated protein 1: a PDZ
 RT domain-containing protein that interacts with BAI1.";
 RL Biochem. Biophys. Res. Commun. 247:597-604(1998).
 CC -!- FUNCTION: LIKELY TO BE A POTENT INHIBITOR OF ANGIOGENESIS IN
 CC BRAIN AND MAY PLAY A SIGNIFICANT ROLE AS A MEDIATOR OF THE P53
 CC SIGNAL IN SUPPRESSION OF GLIOBLASTOMA. MAY FUNCTION IN CELL
 CC ADHESION AND SIGNAL TRANSDUCTION IN THE BRAIN.
 CC -!- SUBUNIT: INTERACTS WITH BAP1.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. LIKELY TO BE
 CC CONCENTRATED AT CELL-CELL ADHESION SITES.
 CC -!- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN BRAIN. REDUCED OR NO
 CC EXPRESSION IS OBSERVED IN SOME GLIOBLASTOMA CELL LINES AND CANCER
 CC TISSUES.
 CC -!- INDUCTION: By p53.
 CC -!- DOMAIN: THE TSP1 REPEATS INHIBIT IN VIVO ANGIOGENESIS IN RAT
 CC CORNEA INDUCED BY BFGF.
 CC -!- SIMILARITY: Belongs to family 2 of G-protein coupled receptors.
 CC -!- SIMILARITY: Contains 5 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 GPS domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB005297; BAA23647.1; -.
 DR PIR; T00026; T00026.
 DR Genew; HGNC:943; BAI1.
 DR MIM; 602682; -.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005911; C:intercellular junction; TAS.
 DR GO; GO:0005515; F:protein binding; TAS.
 DR GO; GO:0007409; P:axonogenesis; TAS.
 DR GO; GO:0007155; P:cell adhesion; TAS.
 DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
 DR GO; GO:0007422; P:peripheral nervous system development; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR InterPro; IPR000203; PKD_cys_rich.
 DR InterPro; IPR000884; TSP1.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF01825; GPS; 1.
 DR Pfam; PF02793; HRM; 1.
 DR Pfam; PF00090; tsp_1; 5.
 DR SMART; SM00303; GPS; 1.
 DR SMART; SM00008; HormR; 1.
 DR SMART; SM00209; TSP1; 5.
 DR PROSITE; PS50221; GPS; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; FALSE_NEG.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; FALSE_NEG.

Qy 300 SWSPWSKWSACGLDCT---HWRSRECS DPAPRNGGEECQGTDLDTNRCTSDLC 349
 :|: || |||| | : | :||: | : || |||| : :||:| |
 Db 469 NWNEWSSWSACSASCSQGRQRTRECNGPS--YGGAECQGHVETRDCLQQC 519

RESULT 2

TSP2_HUMAN

ID TSP2_HUMAN STANDARD; PRT; 1172 AA.
 AC P35442;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Thrombospondin 2 precursor.
 GN THBS2 OR TSP2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94010892; PubMed=8406456;
 RA Labell T.L., Byers P.H.;
 RT "Sequence and characterization of the complete human thrombospondin 2
 RT cDNA: potential regulatory role for the 3' untranslated region."
 RL Genomics 17:225-229(1993).
 RN [2]
 RP SEQUENCE OF 560-1172 FROM N.A.
 RC TISSUE=Fibroblast;
 RX MEDLINE=92217961; PubMed=1559694;
 RA Labell T.L., McGookey Milewicz D.J., Distech C.M., Byers P.H.;
 RT "Thrombospondin II: partial cDNA sequence, chromosome location, and
 RT expression of a second member of the thrombospondin gene family in
 RT humans."
 RL Genomics 12:421-429(1992).
 RN [3]
 RP THROMBOSPONDIN REPEATS DISULFIDE BONDS.
 RX MEDLINE=21588233; PubMed=11590138;
 RA Misenheimer T.M., Hahr A.J., Harms A.C., Annis D.S., Mosher D.F.;
 RT "Disulfide connectivity of recombinant C-terminal region of human
 RT thrombospondin 2."
 RL J. Biol. Chem. 276:45882-45887(2001).
 CC -!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and
 CC cell-to-matrix interactions. Can bind to fibrinogen, fibronectin,
 CC laminin and type V collagen.
 CC -!- SUBUNIT: Homotrimer; disulfide-linked.
 CC -!- SIMILARITY: Belongs to the thrombospondin family.
 CC -!- SIMILARITY: Contains 1 VWFC domain.
 CC -!- SIMILARITY: Contains 3 EGF-like domains.
 CC -!- SIMILARITY: Contains 3 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 7 TSP type-3 domains.
 CC -!- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
 CC -----
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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; L12350; AAA03703.1; -.
DR EMBL; M81339; -; NOT_ANNOTATED_CDS.
DR PIR; A47379; TSHUP2.
DR HSSP; P00740; LEDM.
DR Genew; HGNC:11786; THBS2.
DR MIM; 188061; -.
DR GO; GO:0008201; F:heparin binding; TAS.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR InterPro; IPR003367; tsp_3.
DR InterPro; IPR008859; TSPC.
DR InterPro; IPR003129; TSPN.
DR InterPro; IPR001007; VWF_C.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00090; tsp_1; 3.
DR Pfam; PF02412; tsp_3; 13.
DR Pfam; PF05735; TSPC; 1.
DR Pfam; PF02210; TSPN; 1.
DR Pfam; PF00093; vwc; 1.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00181; EGF; 3.
DR SMART; SM00209; TSP1; 3.
DR SMART; SM00210; TSPN; 1.
DR SMART; SM00214; VWC; 1.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 2.
DR PROSITE; PS50092; TSP1; 3.
DR PROSITE; PS01208; VWFC_1; 1.
DR PROSITE; PS50184; VWFC_2; 1.
KW Glycoprotein; Cell adhesion; Calcium-binding; Heparin-binding; Repeat;
KW EGF-like domain; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 1172 THROMBOSPONDIN 2.
FT DOMAIN 19 215 TSP N-TERMINAL.
FT DOMAIN 19 232 HEPARIN-BINDING (POTENTIAL).
FT DOMAIN 318 375 VWFC.
FT DOMAIN 381 431 TSP TYPE-1 1.
FT DOMAIN 437 492 TSP TYPE-1 2.
FT DOMAIN 494 549 TSP TYPE-1 3.
FT DOMAIN 549 589 EGF-LIKE 1.
FT DOMAIN 590 647 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 648 692 EGF-LIKE 3.
FT DOMAIN 725 760 TSP TYPE-3 1.
FT DOMAIN 761 783 TSP TYPE-3 2.
FT DOMAIN 784 819 TSP TYPE-3 3.
FT DOMAIN 820 842 TSP TYPE-3 4.
FT DOMAIN 843 880 TSP TYPE-3 5.
FT DOMAIN 881 916 TSP TYPE-3 6.
FT DOMAIN 917 952 TSP TYPE-3 7.

FT	DOMAIN	953	1172	C-TERMINAL.
FT	SITE	928	930	CELL ATTACHMENT SITE (POTENTIAL).
FT	DISULFID	266	266	INTERCHAIN (PROBABLE).
FT	DISULFID	270	270	INTERCHAIN (PROBABLE).
FT	DISULFID	393	425	BY SIMILARITY.
FT	DISULFID	397	430	BY SIMILARITY.
FT	DISULFID	408	415	BY SIMILARITY.
FT	DISULFID	449	486	BY SIMILARITY.
FT	DISULFID	453	491	BY SIMILARITY.
FT	DISULFID	464	476	BY SIMILARITY.
FT	DISULFID	506	543	BY SIMILARITY.
FT	DISULFID	510	548	BY SIMILARITY.
FT	DISULFID	521	533	BY SIMILARITY.
FT	DISULFID	553	564	BY SIMILARITY.
FT	DISULFID	558	574	BY SIMILARITY.
FT	DISULFID	577	588	BY SIMILARITY.
FT	DISULFID	594	610	BY SIMILARITY.
FT	DISULFID	601	619	BY SIMILARITY.
FT	DISULFID	622	646	BY SIMILARITY.
FT	DISULFID	652	665	BY SIMILARITY.
FT	DISULFID	659	678	BY SIMILARITY.
FT	DISULFID	680	691	BY SIMILARITY.
FT	DISULFID	707	715	
FT	DISULFID	720	740	
FT	DISULFID	756	776	
FT	DISULFID	779	799	
FT	DISULFID	815	835	
FT	DISULFID	838	858	
FT	DISULFID	876	896	
FT	DISULFID	912	932	
FT	DISULFID	948	1169	
FT	CARBOHYD	151	151	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	316	316	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	330	330	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	457	457	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	584	584	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	710	710	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1069	1069	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	1172 AA;	129955 MW;	2AC7BB230E44C6F5 CRC64;

Query Match 6.2%; Score 296.5; DB 1; Length 1172;
 Best Local Similarity 30.5%; Pred. No. 2.5e-14;
 Matches 78; Conservative 28; Mismatches 105; Indels 45; Gaps 9;

Qy	209	RQARLADTANYTCVAKNIVARRRSASAA-VIVYVNGGWSTWTEWSVCSASCGRGWQKRSR	267
		:: : : : : : : :	
Db	403	QRGRSCDVTSNTCLGPSIQTRACSLSKCDTRIRQDGGWSHSPWSSCSVTGCGVNITRIR	462
Qy	268	SCTNPAPLNGGAFCEGQNVQKTAC-ATLCPVDGWSWSPWSKWSACGLDCT---HWSRECS	323
		: : : : : : :	
Db	463	LCNSPVPQMGGKNCKGSGRETKACQGAPCPIDGRWSPWSPWSACTVTCAGGIRERTRVCN	522
Qy	324	DPAPRNGGEECQGTDLDRNCTSDLCVHSASGPEDVALYVGLIAVAVCLVLLLLVLILVY	383
		: : : :	
Db	523	SPEPQYGGKACVGDVQERQMCNKRSC-----PVDGCLSNPCFPGAQC-----	564
Qy	384	CRKKEGLDSDVADSSILTSGFQPVSI--KPSKADNPHELLTIQPDLSTTTT-----TYQ	434

```

          | | | : || ||      : ::      : ||: :|:      |
Db      565 -----SSFPDGS-WSCGFCPVGFLGNGTHCEDLDECALVPDICFSTSKVPRCVNTQP 615

Qy      435 GSLC----PRQDGPSP 446
          | |      || | |
Db      616 GFHCLPCPPRYRGNQP 631

```

RESULT 3

SM5A_HUMAN

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ID      SM5A_HUMAN      STANDARD;      PRT; 1074 AA.
AC      Q13591; O60408;
DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Semaphorin 5A precursor (Semaphorin F) (Sema F).
GN      SEMA5A OR SEMAF.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98125554; PubMed=9464278;
RA      Simmons A.D., Puschel A.W., McPherson J.D., Overhauser J., Lovett M.;
RT      "Molecular cloning and mapping of human semaphorin F from the Cri-du-
RT      chat candidate interval.";
RL      Biochem. Biophys. Res. Commun. 242:685-691(1998).
RN      [2]
RP      SEQUENCE OF 1-494 FROM N.A.
RA      Kalicki J., Harmon G.;
RL      Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
CC      -!- FUNCTION: May act as positive axonal guidance cues.
CC      -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -!- SIMILARITY: Belongs to the semaphorin family.
CC      -!- SIMILARITY: Contains 1 Sema domain.
CC      -!- SIMILARITY: Contains 7 TSP type-1 domains.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U52840; AAC09473.1; -.
DR      EMBL; AC004615; AAC14668.1; -.
DR      PIR; JC5928; JC5928.
DR      Genew; HGNC:10736; SEMA5A.
DR      GO; GO:0007155; P:cell adhesion; TAS.
DR      GO; GO:0007267; P:cell-cell signaling; TAS.
DR      GO; GO:0007399; P:neurogenesis; TAS.
DR      InterPro; IPR003659; Plexin-like.
DR      InterPro; IPR002165; Plexin_repeat.
DR      InterPro; IPR001627; Sema.
DR      InterPro; IPR000884; TSP1.

```


AC Q03350;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Thrombospondin 2 precursor.
 GN THBS2 OR TSP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92147683; PubMed=1371115;
 RA Laherty C.D., O'Rourke K., Wolf F.W., Katz R., Seldin M.F.,
 RA Dixit V.M.;
 RT "Characterization of mouse thrombospondin 2 sequence and expression
 RT during cell growth and development.";
 RL J. Biol. Chem. 267:3274-3281(1992).
 RN [2]
 RP SEQUENCE OF 1-873 FROM N.A.
 RX MEDLINE=91302287; PubMed=1712771;
 RA Bornstein P., O'Rourke K., Wikstrom K., Wolf F.W., Katz R., Li P.,
 RA Dixit V.M.;
 RT "A second, expressed thrombospondin gene (Thbs2) exists in the mouse
 RT genome.";
 RL J. Biol. Chem. 266:12821-12824(1991).
 CC -!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and
 CC cell-to-matrix interactions. Can bind to fibrinogen, fibronectin,
 CC laminin and type V collagen.
 CC -!- SUBUNIT: Homotrimer; disulfide-linked.
 CC -!- SIMILARITY: Belongs to the thrombospondin family.
 CC -!- SIMILARITY: Contains 1 VWFC domain.
 CC -!- SIMILARITY: Contains 3 EGF-like domains.
 CC -!- SIMILARITY: Contains 3 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 7 TSP type-3 domains.
 CC -!- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L07803; AAA53064.1; -.
 DR EMBL; M64866; AAA40432.1; -.
 DR PIR; A42587; A42587.
 DR HSSP; P00740; 1EDM.
 DR MGD; MGI:98738; Thbs2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR003367; tsp_3.
 DR InterPro; IPR008859; TSPC.

DR InterPro; IPR003129; TSPN.
 DR InterPro; IPR001007; VWF_C.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00090; tsp_1; 3.
 DR Pfam; PF02412; tsp_3; 13.
 DR Pfam; PF05735; TSPC; 1.
 DR Pfam; PF02210; TSPN; 1.
 DR Pfam; PF00093; vwc; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00181; EGF; 3.
 DR SMART; SM00209; TSP1; 3.
 DR SMART; SM00210; TSPN; 1.
 DR SMART; SM00214; VWC; 1.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50026; EGF_3; 2.
 DR PROSITE; PS50092; TSP1; 3.
 DR PROSITE; PS01208; VWFC_1; 1.
 DR PROSITE; PS50184; VWFC_2; 1.
 KW Glycoprotein; Cell adhesion; Calcium-binding; Heparin-binding; Repeat;
 KW EGF-like domain; Signal.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 1172 THROMBOSPONDIN 2.
 FT DOMAIN 19 215 TSP N-TERMINAL.
 FT DOMAIN 19 232 HEPARIN-BINDING (POTENTIAL).
 FT DOMAIN 318 375 VWFC.
 FT DOMAIN 381 431 TSP TYPE-1 1.
 FT DOMAIN 437 492 TSP TYPE-1 2.
 FT DOMAIN 494 549 TSP TYPE-1 3.
 FT DOMAIN 549 589 EGF-LIKE 1.
 FT DOMAIN 590 647 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 648 692 EGF-LIKE 3.
 FT DOMAIN 725 760 TSP TYPE-3 1.
 FT DOMAIN 761 783 TSP TYPE-3 2.
 FT DOMAIN 784 819 TSP TYPE-3 3.
 FT DOMAIN 820 842 TSP TYPE-3 4.
 FT DOMAIN 843 880 TSP TYPE-3 5.
 FT DOMAIN 881 916 TSP TYPE-3 6.
 FT DOMAIN 917 952 TSP TYPE-3 7.
 FT DOMAIN 953 1172 C-TERMINAL.
 FT SITE 928 930 CELL ATTACHMENT SITE (POTENTIAL).
 FT DISULFID 266 266 INTERCHAIN (PROBABLE).
 FT DISULFID 270 270 INTERCHAIN (PROBABLE).
 FT DISULFID 393 425 BY SIMILARITY.
 FT DISULFID 397 430 BY SIMILARITY.
 FT DISULFID 408 415 BY SIMILARITY.
 FT DISULFID 449 486 BY SIMILARITY.
 FT DISULFID 453 491 BY SIMILARITY.
 FT DISULFID 464 476 BY SIMILARITY.
 FT DISULFID 506 543 BY SIMILARITY.
 FT DISULFID 510 548 BY SIMILARITY.
 FT DISULFID 521 533 BY SIMILARITY.
 FT DISULFID 553 564 BY SIMILARITY.
 FT DISULFID 558 574 BY SIMILARITY.
 FT DISULFID 577 588 BY SIMILARITY.
 FT DISULFID 594 610 BY SIMILARITY.
 FT DISULFID 601 619 BY SIMILARITY.

FT	DISULFID	622	646	BY SIMILARITY.
FT	DISULFID	652	665	BY SIMILARITY.
FT	DISULFID	659	678	BY SIMILARITY.
FT	DISULFID	680	691	BY SIMILARITY.
FT	DISULFID	707	715	BY SIMILARITY.
FT	DISULFID	720	740	BY SIMILARITY.
FT	DISULFID	756	776	BY SIMILARITY.
FT	DISULFID	779	799	BY SIMILARITY.
FT	DISULFID	815	835	BY SIMILARITY.
FT	DISULFID	838	858	BY SIMILARITY.
FT	DISULFID	876	896	BY SIMILARITY.
FT	DISULFID	912	932	BY SIMILARITY.
FT	DISULFID	948	1169	BY SIMILARITY.
FT	CARBOHYD	151	151	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	316	316	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	330	330	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	457	457	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	584	584	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	710	710	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1069	1069	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	1172 AA;	129911 MW;	7CE8E4E8599822AB CRC64;

Query Match 6.1%; Score 293; DB 1; Length 1172;
 Best Local Similarity 38.0%; Pred. No. 4.7e-14;
 Matches 60; Conservative 22; Mismatches 66; Indels 10; Gaps 5;

Qy	209	RQARLADTANYTCVAKNIVARRRS-ASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSR	267
		:: : : : : : :	
Db	403	QRGRSCDVTSTNTCLGPSIQTRTCSLKGCDTRIRQNGGWSHWSPWSSCSVTCGVGNVTRIR	462
Qy	268	SCTNPAPLNGGAFCEGQNVQKTAC-ATLCPVDGWSWSPWSKWSACGLDCT---HWSRSRECS	323
		: : : : : :	
Db	463	LCNSPVPQMGGKNCKGSGRETQPCQRPIDGRWSPWSPWSACTVTCAGGIRERSRVCN	522
Qy	324	DPAPRNGGEECQG--TD---LDTRNCTSDLCVHSASGP	356
		: : : : : : :	
Db	523	SPEPQYGGKDCVGDVTEHQMCNKRSCPIDGCLSNPCFP	560

RESULT 5

TSP2_BOVIN

ID	TSP2_BOVIN	STANDARD;	PRT; 1170 AA.
AC	Q95116; Q28180;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	15-JUL-1999 (Rel. 38, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Thrombospondin 2 precursor (Corticotropin-induced secreted protein)		
DE	(CISP).		
GN	THBS2 OR TSP2 OR TSP-2.		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;		
OC	Bovidae; Bovinae; Bos.		
OX	NCBI_TaxID=9913;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Danik M., Chinn A., Lafeuillade M., Keramidas M., Aguesse-Germon S.,		

RA Penhoat A., Chen H., Mosher D., Chambaz E.M., Feige J.J.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE OF 1-522 FROM N.A.
 RX MEDLINE=96331130; PubMed=8698834;
 RA Lafeuillade B., Pellerin S., Keramidas M., Danik M., Chambaz E.M.,
 RA Feige J.J.;
 RT "Opposite regulation of thrombospondin-1 and corticotropin-induced
 RT secreted protein/thrombospondin-2 expression by adrenocorticotrophic
 RT hormone in adrenocortical cells.";
 RL J. Cell. Physiol. 167:164-172(1996).
 RN [3]
 RP SEQUENCE OF 318-831 FROM N.A.
 RC TISSUE=Aortic endothelium;
 RA Zafar R.S., Moll Y.D., Womack J.F., Walz D.A.;
 RT "Cloning and sequencing of bovine thrombospondin stimulatory effect of
 RT TGF-beta.";
 RL Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and
 CC cell-to-matrix interactions. Can bind to fibrinogen, fibronectin,
 CC laminin and type V collagen.
 CC -!- SUBUNIT: Homotrimer; disulfide-linked.
 CC -!- SIMILARITY: Belongs to the thrombospondin family.
 CC -!- SIMILARITY: Contains 1 VWFC domain.
 CC -!- SIMILARITY: Contains 3 EGF-like domains.
 CC -!- SIMILARITY: Contains 3 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 7 TSP type-3 domains.
 CC -!- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
 CC -----
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 CC -----
 DR EMBL; X96540; CAA65385.1; -.
 DR EMBL; X87620; CAA60952.1; -.
 DR HSSP; P00740; 1EDM.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR003367; tsp_3.
 DR InterPro; IPR008859; TSPC.
 DR InterPro; IPR003129; TSPN.
 DR InterPro; IPR001007; VWF_C.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00090; tsp_1; 3.
 DR Pfam; PF02412; tsp_3; 13.
 DR Pfam; PF05735; TSPC; 1.
 DR Pfam; PF02210; TSPN; 1.
 DR Pfam; PF00093; vwc; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00181; EGF; 3.

DR SMART; SM00209; TSP1; 3.
 DR SMART; SM00210; TSPN; 1.
 DR SMART; SM00214; VWC; 1.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50026; EGF_3; 2.
 DR PROSITE; PS50092; TSP1; 3.
 DR PROSITE; PS01208; VWFC_1; 1.
 DR PROSITE; PS50184; VWFC_2; 1.
 KW Glycoprotein; Cell adhesion; Calcium-binding; Heparin-binding; Repeat;
 KW EGF-like domain; Signal.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 1170 THROMBOSPONDIN 2.
 FT DOMAIN 19 215 TSP N-TERMINAL.
 FT DOMAIN 19 232 HEPARIN-BINDING (POTENTIAL).
 FT DOMAIN 318 375 VWFC.
 FT DOMAIN 379 429 TSP TYPE-1 1.
 FT DOMAIN 435 490 TSP TYPE-1 2.
 FT DOMAIN 492 547 TSP TYPE-1 3.
 FT DOMAIN 547 587 EGF-LIKE 1.
 FT DOMAIN 588 645 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 646 690 EGF-LIKE 3.
 FT DOMAIN 723 758 TSP TYPE-3 1.
 FT DOMAIN 759 781 TSP TYPE-3 2.
 FT DOMAIN 782 817 TSP TYPE-3 3.
 FT DOMAIN 818 840 TSP TYPE-3 4.
 FT DOMAIN 841 878 TSP TYPE-3 5.
 FT DOMAIN 879 914 TSP TYPE-3 6.
 FT DOMAIN 915 950 TSP TYPE-3 7.
 FT DOMAIN 951 1170 C-TERMINAL.
 FT SITE 926 928 CELL ATTACHMENT SITE (POTENTIAL).
 FT DISULFID 266 266 INTERCHAIN (PROBABLE).
 FT DISULFID 270 270 INTERCHAIN (PROBABLE).
 FT DISULFID 391 423 BY SIMILARITY.
 FT DISULFID 395 428 BY SIMILARITY.
 FT DISULFID 406 413 BY SIMILARITY.
 FT DISULFID 447 484 BY SIMILARITY.
 FT DISULFID 451 489 BY SIMILARITY.
 FT DISULFID 462 474 BY SIMILARITY.
 FT DISULFID 504 541 BY SIMILARITY.
 FT DISULFID 508 546 BY SIMILARITY.
 FT DISULFID 519 531 BY SIMILARITY.
 FT DISULFID 551 562 BY SIMILARITY.
 FT DISULFID 556 572 BY SIMILARITY.
 FT DISULFID 575 586 BY SIMILARITY.
 FT DISULFID 592 608 BY SIMILARITY.
 FT DISULFID 599 617 BY SIMILARITY.
 FT DISULFID 620 644 BY SIMILARITY.
 FT DISULFID 650 663 BY SIMILARITY.
 FT DISULFID 657 676 BY SIMILARITY.
 FT DISULFID 678 689 BY SIMILARITY.
 FT DISULFID 705 713 BY SIMILARITY.
 FT DISULFID 718 738 BY SIMILARITY.
 FT DISULFID 754 774 BY SIMILARITY.
 FT DISULFID 777 797 BY SIMILARITY.
 FT DISULFID 813 833 BY SIMILARITY.
 FT DISULFID 836 856 BY SIMILARITY.

FT	DISULFID	874	894	BY SIMILARITY.
FT	DISULFID	910	930	BY SIMILARITY.
FT	DISULFID	946	1167	BY SIMILARITY.
FT	CARBOHYD	151	151	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	316	316	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	330	330	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	455	455	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	582	582	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	708	708	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	936	936	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1067	1067	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	535	535	A -> V (IN REF. 3).
FT	CONFLICT	748	748	S -> T (IN REF. 3).
SQ	SEQUENCE	1170 AA;	129862 MW;	9CF1FBF55B89A051 CRC64;

Query Match 6.1%; Score 291.5; DB 1; Length 1170;
 Best Local Similarity 38.4%; Pred. No. 6.1e-14;
 Matches 56; Conservative 21; Mismatches 64; Indels 5; Gaps 3;

Qy	209	RQARLADTANYTCVAKNIVARRRSASAA-VIVYVNGGWSTWTEWSVCSASCGRGWQKRSR	267
		: : : : : : : :	
Db	401	QRGRSCDVTSNTCLGPSIQTRACSLGRCDHRIRQDGGWSHWSPWSSCSVTCGVGNVTRIR	460
Qy	268	SCTNPAPLNGGAFCEGQNVQKTAC-ATLCPVDGWSWPWSKWSACGLDCT---HWSRECS	323
		: : : : : :	
Db	461	LCNSPVPQMGGRSCKGSGRETKACQGPPCPVDGRWSPWSPWSACTVTCAGGIRERTRVCN	520
Qy	324	DPAPRNGGEECQGTDLDRNCTSDLC	349
		: : : :	
Db	521	SPEPQHGGKDCVGGAKEQQMCNRKSC	546

RESULT 6

SM5A_MOUSE

ID SM5A_MOUSE STANDARD; PRT; 1077 AA.
 AC Q62217;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Semaphorin 5A precursor (Semaphorin F) (Sema F).
 GN SEMA5A OR SEMAF OR SEMF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NMRI;
 RX MEDLINE=96414430; PubMed=8817451;
 RA Adams R.H., Betz H., Pueschel A.W.;
 RT "A novel class of murine semaphorins with homology to thrombospondin
 RT is differentially expressed during early embryogenesis.";
 RL Mech. Dev. 57:33-45(1996).
 CC -!- FUNCTION: May act as positive axonal guidance cues.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: IN ADULT, DETECTED IN LIVER, BRAIN, KIDNEY,
 CC HEART, LUNG AND SPLEEN.

```

CC  -!- DEVELOPMENTAL STAGE: DIFFERENTIALLY EXPRESSED IN EMBRYONIC AND
CC      ADULT TISSUES. ITS ABUNDANCE DECREASES FROM E10 TO BIRTH.
CC  -!- SIMILARITY: Belongs to the semaphorin family.
CC  -!- SIMILARITY: Contains 1 Sema domain.
CC  -!- SIMILARITY: Contains 7 TSP type-1 domains.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; X97817; CAA66397.1; -.
DR  MGD; MGI:107556; Sema5a.
DR  GO; GO:0016021; C:integral to membrane; IDA.
DR  GO; GO:0008046; F:axon guidance receptor activity; IDA.
DR  GO; GO:0007411; P:axon guidance; IMP.
DR  InterPro; IPR003659; Plexin-like.
DR  InterPro; IPR002165; Plexin_repeat.
DR  InterPro; IPR001627; Sema.
DR  InterPro; IPR000884; TSP1.
DR  InterPro; IPR008085; TSP_1.
DR  Pfam; PF01437; PSI; 1.
DR  Pfam; PF01403; Sema; 1.
DR  Pfam; PF00090; tsp_1; 5.
DR  PRINTS; PR01705; TSP1REPEAT.
DR  SMART; SM00423; PSI; 1.
DR  SMART; SM00630; Sema; 1.
DR  SMART; SM00209; TSP1; 6.
DR  PROSITE; PS50092; TSP1; 6.
KW  Signal; Transmembrane; Repeat; Multigene family; Neurogenesis;
KW  Developmental protein; Glycoprotein.
FT  SIGNAL          1      21      POTENTIAL.
FT  CHAIN           22     1077    SEMAPHORIN 5A.
FT  DOMAIN          22     971     EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM        972     992     POTENTIAL.
FT  DOMAIN          993    1077    CYTOPLASMIC (POTENTIAL).
FT  DOMAIN          226     507     SEMA.
FT  DOMAIN          540     593     TSP TYPE-1 1.
FT  DOMAIN          595     651     TSP TYPE-1 2.
FT  DOMAIN          653     702     TSP TYPE-1 3.
FT  DOMAIN          707     765     TSP TYPE-1 4.
FT  DOMAIN          784     839     TSP TYPE-1 5.
FT  DOMAIN          841     896     TSP TYPE-1 6.
FT  DOMAIN          897     944     TSP TYPE-1 7.
FT  CARBOHYD        147     147     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD        168     168     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD        227     227     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD        277     277     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD        323     323     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD        367     367     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD        536     536     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD        591     591     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD        717     717     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD        933     933     N-LINKED (GLCNAC. . .) (POTENTIAL).

```

SQ SEQUENCE 1077 AA; 120826 MW; EDAB0DDDA42789FF CRC64;

Query Match 6.1%; Score 291; DB 1; Length 1077;

Best Local Similarity 45.8%; Pred. No. 5.9e-14;

Matches 54; Conservative 10; Mismatches 50; Indels 4; Gaps 2;

```
Qy      241 VNGGWSTWTEWSVCSASCGRGWQKRSRSCNPPAPLNGGAFCEGQNVQKTACATL-CPVDG 299
          ||| || || || || | || : | | | || | || | | :: | | ||||
Db      783 VNGAWSAWTSWSQCSRDCSRGI RNRKRVCNNPEPKFGGMPCLGPSLEFQECNILPCPVDG 842

Qy      300 SWSPWSKWSACGLDC---THWRSRECSDPAPRNGGEECQGTDLDTNRCTSDLCVHSAS 354
          || || || | | : | : | || || || : | | : | | |
Db      843 VWSCWSSWSKCSATCGGGHYMRTRSCSNPAPAYGGDICLGLHTEEALCNTQTCPEWS 900
```

RESULT 7

TSP1_XENLA

ID TSP1_XENLA STANDARD; PRT; 1173 AA.

AC P35448;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Thrombospondin 1 precursor.

GN THBS1 OR TSP1.

OS *Xenopus laevis* (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

OC Xenopodinae; *Xenopus*.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RA Urry L.A., Ramos J., Duquette M., Desimone D.W., Lawler J.;

RL Submitted (XXX-1993) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and
CC cell-to-matrix interactions. Can bind to fibrinogen, fibronectin,
CC laminin, type V collagen and integrins alpha-V/beta-1, alpha-
CC V/beta-3 and alpha-IIb/beta-3 (By similarity).

CC -!- SUBUNIT: Homotrimer; disulfide-linked.

CC -!- SIMILARITY: Belongs to the thrombospondin family.

CC -!- SIMILARITY: Contains 1 VWFC domain.

CC -!- SIMILARITY: Contains 3 EGF-like domains.

CC -!- SIMILARITY: Contains 3 TSP type-1 domains.

CC -!- SIMILARITY: Contains 7 TSP type-3 domains.

CC -!- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.

CC -----
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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; L04278; -; NOT_ANNOTATED_CDS.

DR HSSP; P00740; 1EDM.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR006209; EGF_like.

DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR003367; tsp_3.
 DR InterPro; IPR008859; TSPC.
 DR InterPro; IPR003129; TSPN.
 DR InterPro; IPR001007; VWF_C.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00090; tsp_1; 3.
 DR Pfam; PF02412; tsp_3; 13.
 DR Pfam; PF05735; TSPC; 1.
 DR Pfam; PF02210; TSPN; 1.
 DR Pfam; PF00093; vwc; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00209; TSP1; 3.
 DR SMART; SM00210; TSPN; 1.
 DR SMART; SM00214; VWC; 1.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50026; EGF_3; 2.
 DR PROSITE; PS50092; TSP1; 3.
 DR PROSITE; PS01208; VWFC_1; 1.
 DR PROSITE; PS50184; VWFC_2; 1.
 KW Glycoprotein; Cell adhesion; Calcium-binding; Heparin-binding; Repeat;
 KW EGF-like domain; Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 1173 THROMBOSPONDIN 1.
 FT DOMAIN 23 235 HEPARIN-BINDING (POTENTIAL).
 FT DOMAIN 23 224 TSP N-TERMINAL.
 FT DOMAIN 319 376 VWFC.
 FT DOMAIN 382 432 TSP TYPE-1 1.
 FT DOMAIN 438 493 TSP TYPE-1 2.
 FT DOMAIN 495 550 TSP TYPE-1 3.
 FT DOMAIN 550 590 EGF-LIKE 1.
 FT DOMAIN 591 648 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 649 693 EGF-LIKE 3.
 FT DOMAIN 726 761 TSP TYPE-3 1.
 FT DOMAIN 762 784 TSP TYPE-3 2.
 FT DOMAIN 785 820 TSP TYPE-3 3.
 FT DOMAIN 821 843 TSP TYPE-3 4.
 FT DOMAIN 844 881 TSP TYPE-3 5.
 FT DOMAIN 882 917 TSP TYPE-3 6.
 FT DOMAIN 918 953 TSP TYPE-3 7.
 FT DOMAIN 954 1173 C-TERMINAL.
 FT SITE 929 931 CELL ATTACHMENT SITE (POTENTIAL).
 FT DISULFID 394 426 BY SIMILARITY.
 FT DISULFID 398 431 BY SIMILARITY.
 FT DISULFID 409 416 BY SIMILARITY.
 FT DISULFID 450 487 BY SIMILARITY.
 FT DISULFID 454 492 BY SIMILARITY.
 FT DISULFID 465 477 BY SIMILARITY.
 FT DISULFID 507 544 BY SIMILARITY.
 FT DISULFID 511 549 BY SIMILARITY.
 FT DISULFID 522 534 BY SIMILARITY.
 FT DISULFID 554 565 BY SIMILARITY.
 FT DISULFID 559 575 BY SIMILARITY.

FT	DISULFID	578	589	BY SIMILARITY.
FT	DISULFID	595	611	BY SIMILARITY.
FT	DISULFID	602	620	BY SIMILARITY.
FT	DISULFID	623	647	BY SIMILARITY.
FT	DISULFID	653	666	BY SIMILARITY.
FT	DISULFID	660	679	BY SIMILARITY.
FT	DISULFID	681	692	BY SIMILARITY.
FT	DISULFID	708	716	BY SIMILARITY.
FT	DISULFID	721	741	BY SIMILARITY.
FT	DISULFID	757	777	BY SIMILARITY.
FT	DISULFID	780	800	BY SIMILARITY.
FT	DISULFID	816	836	BY SIMILARITY.
FT	DISULFID	839	859	BY SIMILARITY.
FT	DISULFID	877	897	BY SIMILARITY.
FT	DISULFID	913	933	BY SIMILARITY.
FT	DISULFID	949	1170	BY SIMILARITY.
FT	CARBOHYD	155	155	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	158	158	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	250	250	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	363	363	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	705	705	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	711	711	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1070	1070	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	1173 AA;	130019 MW;	A9F036D6516C0F24 CRC64;

Query Match 6.1%; Score 290; DB 1; Length 1173;
 Best Local Similarity 24.2%; Pred. No. 7.9e-14;
 Matches 92; Conservative 52; Mismatches 144; Indels 92; Gaps 16;

Qy	11	LLGIVLAAWLRGSG----	AQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKPVLLVCK	66
		:	: : : : :	
Db	221	VFGTTLEAILRNKGCLSMNSVITLDPNVNGSSPAIRTNYIGH-----	KTKDLQAVCG	273
Qy	67	AVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRRQVEKVFGLLEEYWCQC	126	
		: : : : :		
Db	274	-----FSCDD-----LSKLEAEMKGLRTL---VTTLKDQVTKETEKNELIAQI	313	
Qy	127	VAWSSSGT'TKSQKAYIRIARLRKNFEQ-----	EPLAKEVSLEQGIVLPCRP	172
		: : : : : : : : :		
Db	314	V-----TRTPGVCLHNGVLHKNRDEWTVDSCTECTCQNSATICRKVSCP---	LMPCTN	363
Qy	173	---PEG-----IPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTC	221	
		: : : : : : :		
Db	364	ATIPDGECCPRCWPSDSADDDWSPWSDWTPCS-----	VTCGHG-IQQRGRSCDSLNNPC	416
Qy	222	VAKNIVAR-----RRSASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCNPA	273	
		: : : : : :		
Db	417	EGSSVQTRSCQIQDCDKRFKQ-----	DGGWSHWPWSSCSVTGSGQITRIRLCNSPV	469
Qy	274	PLNGGAFCEGQNVQKTAC-ATLCPVDGWSWPWSKWSACGLDC---	THWRSRECSDPAPRN	329
		: : : :		
Db	470	PQLNGKQCEGEGRENKPCQKDPINGQWGPWSLWDTCTVTCGGGMQKRERLCNNPKPQY	529	
Qy	330	GGEECQGTDLDTNRNCTSDLC	349	
		: :		
Db	530	EGKDCIGEPTDSQICNKQDC	549	

RESULT 8

SM5B_HUMAN

ID SM5B_HUMAN STANDARD; PRT; 1093 AA.
AC Q9P283;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Semaphorin 5B precursor.
GN SEMA5B OR KIAA1445.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20277482; PubMed=10819331;
RA Nagase T., Kikuno R., Ishikawa K.-I., Hirose M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XVII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 7:143-150(2000).
CC -!- FUNCTION: May act as positive axonal guidance cues (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the semaphorin family.
CC -!- SIMILARITY: Contains 1 Sema domain.
CC -!- SIMILARITY: Contains 7 TSP type-1 domains.
CC -----
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CC -----
DR EMBL; AB040878; BAA95969.1; ALT_INIT.
DR Genew; HGNC:10737; SEMA5B.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR InterPro; IPR001627; Sema.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR Pfam; PF01437; PSI; 1.
DR Pfam; PF01403; Sema; 1.
DR Pfam; PF00090; tsp_1; 5.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00630; Sema; 1.
DR SMART; SM00209; TSP1; 4.
DR PROSITE; PS50092; TSP1; 5.
KW Signal; Transmembrane; Repeat; Multigene family; Neurogenesis;
KW Developmental protein; Glycoprotein.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 1093 SEMAPHORIN 5B.

FT	DOMAIN	20	978	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	979	999	POTENTIAL.
FT	DOMAIN	1000	1093	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	236	518	SEMA.
FT	DOMAIN	551	605	TSP TYPE-1 1.
FT	DOMAIN	606	662	TSP TYPE-1 2.
FT	DOMAIN	664	713	TSP TYPE-1 3.
FT	DOMAIN	721	776	TSP TYPE-1 4.
FT	DOMAIN	795	850	TSP TYPE-1 5.
FT	DOMAIN	852	907	TSP TYPE-1 6.
FT	DOMAIN	908	952	TSP TYPE-1 7.
FT	CARBOHYD	59	59	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	95	95	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	157	157	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	178	178	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	287	287	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	333	333	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	378	378	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	532	532	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	539	539	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	547	547	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	602	602	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	728	728	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	944	944	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	1093 AA; 119866 MW; F1FDEFB87CEAF0EF CRC64;		

Query Match 5.8%; Score 276; DB 1; Length 1093;
 Best Local Similarity 31.0%; Pred. No. 8.4e-13;
 Matches 72; Conservative 35; Mismatches 79; Indels 46; Gaps 11;

Qy	241	VNGGWSTWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACAT-LCPVDG	299
		: : : : :	
Db	851	VRGAWSCWTSWSPCSASC GG GHYQRTSRCTSPAPSPGEDICLGLHTEALCATQACP--E	908
Qy	300	SWSPWSKWSACGLDCTHWSRECS DPAPRNGGEECQGTDL DTRNCT-SDL-CVHSASGPE	357
		: : : : :	
Db	909	GWSPWSEWSKCTDDGAQSRSRHCEELP---GSSACAGNSSQSRPCPYSEIPVILPASSME	966
Qy	358	DVALYVG-----LIAVAVCLVL---LLLVLILVYCR--KKEGLDSDVADSSILTSGFQPV	407
		: : : : : : : : : :	
Db	967	EATGCAGFNLIHLVATGISCF LGSGLLT LAVYLS CQHCQRQSQESTL-----	1013
Qy	408	SIKPSKADNPHELLTIQPD LSTTTTTTYQGS LCP RQDGPSP-KFQLTNGHLLSP	458
		: : : : : : : : : :	
Db	1014	-VHPATPNHLH-----YKGGGTPKNEKYTPMEFKTLNKNNLIP	1050

RESULT 9

SM5B_MOUSE

ID SM5B_MOUSE STANDARD; PRT; 1093 AA.
 AC Q60519;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Semaphorin 5B precursor (Semaphorin G) (Sema G).
 GN SEMA5B OR SEMAG OR SEMG.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NMRI;
 RX MEDLINE=96414430; PubMed=8817451;
 RA Adams R.H., Betz H., Pueschel A.W.;
 RT "A novel class of murine semaphorins with homology to thrombospondin
 RT is differentially expressed during early embryogenesis.";
 RL Mech. Dev. 57:33-45(1996).
 CC -!- FUNCTION: May act as positive axonal guidance cues.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: In adult, only detected in brain.
 CC -!- DEVELOPMENTAL STAGE: Differentially expressed in embryonic and
 CC adult tissues. Its abundance decreases from E10 to birth.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -!- SIMILARITY: Contains 7 TSP type-1 domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X97818; CAA66398.1; -.
 DR MGD; MGI:107555; Sema5b.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR Pfam; PF00090; tsp_1; 5.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR SMART; SM00209; TSP1; 4.
 DR PROSITE; PS50092; TSP1; 5.
 KW Signal; Transmembrane; Repeat; Multigene family; Neurogenesis;
 KW Developmental protein; Glycoprotein.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 1093 SEMAPHORIN 5B.
 FT DOMAIN 20 978 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 979 999 POTENTIAL.
 FT DOMAIN 1000 1093 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 236 518 SEMA.
 FT DOMAIN 551 605 TSP TYPE-1 1.
 FT DOMAIN 606 662 TSP TYPE-1 2.
 FT DOMAIN 664 713 TSP TYPE-1 3.
 FT DOMAIN 721 776 TSP TYPE-1 4.
 FT DOMAIN 795 850 TSP TYPE-1 5.
 FT DOMAIN 852 907 TSP TYPE-1 6.

FT	DOMAIN	908	952	TSP TYPE-1 7.
FT	CARBOHYD	59	59	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	95	95	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	157	157	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	178	178	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	287	287	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	333	333	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	378	378	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	532	532	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	539	539	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	547	547	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	602	602	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	728	728	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	944	944	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	1093 AA; 120326 MW; 29E5C9B1E8108717 CRC64;		

Query Match 5.8%; Score 275.5; DB 1; Length 1093;
 Best Local Similarity 32.1%; Pred. No. 9.2e-13;
 Matches 69; Conservative 18; Mismatches 75; Indels 53; Gaps 8;

Qy	163	EQGIVLPCRPPGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCV	222
Db	737	EQRFRFTCRAP-----LPDP-----HGLQFGKRR---TETRTCP	767
Qy	223	AKNIVA-----RRRSASAAVIVVNGGWSTWTEWSVCSASCGRGWQKRSRSTN	271
Db	768	ADGTGACDLDALVEDLLRSGSTSPHTL---NGGWATWGPWSSCSRDCELGFRVRKRTCTN	824
Qy	272	PAPLNGGAFCEGQNVQKTAC-ATLCPVDGWSWPSKWSACGLDC---THWRSRECSDPAP	327
Db	825	PEPRNGGLPCVGDAAEYQDCNPQACPVRGAWSCWTAWSQCSASC GG GGHYQRTSRCTSPAP	884
Qy	328	RNGGEECQGTDLDTNRCTSDLCVHSASGPEDVALY	362
		: : : :	
Db	885	SPGEDICLGLHTEELCSTQAC-----PEGWSLW	913

RESULT 10

BAI3_HUMAN

ID BAI3_HUMAN STANDARD; PRT; 1522 AA.
 AC O60242; O60297;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Brain-specific angiogenesis inhibitor 3 precursor.
 GN BAI3 OR KIAA0550.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=98194217; PubMed=9533023;
 RA Shiratsuchi T., Nishimori H., Ichise H., Nakamura Y., Tokino T.;
 RT "Cloning and characterization of BAI2 and BAI3, novel genes homologous
 to brain-specific angiogenesis inhibitor 1 (BAI1).";

RL Cytogenet. Cell Genet. 79:103-108(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98290545; PubMed=9628581;
 RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
 RA Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. IX.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 5:31-39(1998).
 RN [3]
 RP SEQUENCE FROM N.A., AND REVISIONS TO 643-665 AND C-TERMINUS.
 RX MEDLINE=22158633; PubMed=12168954;
 RA Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;
 RT "Construction of expression-ready cDNA clones for KIAA genes: manual
 RT curation of 330 KIAA cDNA clones.";
 RL DNA Res. 9:99-106(2002).
 CC -!- FUNCTION: MIGHT BE INVOLVED IN ANGIOGENESIS INHIBITION AND
 CC SUPPRESSION OF GLIOBLASTOMA.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN BRAIN. ALSO DETECTED IN
 CC HEART. REDUCED EXPRESSION IS OBSERVED IN SOME GLIOBLASTOMA CELL
 CC LINES.
 CC -!- SIMILARITY: Belongs to family 2 of G-protein coupled receptors.
 CC -!- SIMILARITY: Contains 1 CUB domain.
 CC -!- SIMILARITY: Contains 4 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 GPS domain.
 CC -----
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 CC -----
 DR EMBL; AB005299; BAA25363.1; -.
 DR EMBL; AB011122; BAA25476.2; ALT_INIT.
 DR PIR; T00028; T00028.
 DR Genew; HGNC:945; BAI3.
 DR MIM; 602684; -.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR InterPro; IPR000203; PKD_cys_rich.
 DR InterPro; IPR000884; TSP1.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF01825; GPS; 1.
 DR Pfam; PF02793; HRM; 1.
 DR Pfam; PF00090; tsp_1; 4.
 DR SMART; SM00303; GPS; 1.
 DR SMART; SM00008; HormR; 1.
 DR SMART; SM00209; TSP1; 4.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS50221; GPS; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; FALSE_NEG.

Qy 330 GGEQCQGTDLDRNCTSDLCVHSASG 355
 || ||:| ::| | : | :|:|
 Db 433 GGSECRGPWAESRECYNPEC--TANG 456

RESULT 11

BAI2_HUMAN

ID BAI2_HUMAN STANDARD; PRT; 1572 AA.
 AC O60241;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Brain-specific angiogenesis inhibitor 2 precursor.
 GN BAI2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=98194217; PubMed=9533023;
 RA Shiratsuchi T., Nishimori H., Ichise H., Nakamura Y., Tokino T.;
 RT "Cloning and characterization of BAI2 and BAI3, novel genes homologous
 RT to brain-specific angiogenesis inhibitor 1 (BAI1).";
 RL Cytogenet. Cell Genet. 79:103-108(1997).
 CC -!- FUNCTION: MIGHT BE INVOLVED IN ANGIOGENESIS INHIBITION.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN BRAIN. ALSO DETECTED IN
 CC HEART, THYMUS, SKELETAL MUSCLE, AND DIFFERENT CELL LINES.
 CC -!- SIMILARITY: Belongs to family 2 of G-protein coupled receptors.
 CC -!- SIMILARITY: Contains 4 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 GPS domain.
 CC -----
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 CC -----
 DR EMBL; AB005298; BAA25362.1; -.
 DR PIR; T00027; T00027.
 DR Genew; HGNC:944; BAI2.
 DR MIM; 602683; -.
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR InterPro; IPR000203; PKD_cys_rich.
 DR InterPro; IPR000884; TSP1.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF01825; GPS; 1.
 DR Pfam; PF02793; HRM; 1.
 DR Pfam; PF00090; tsp_1; 4.
 DR SMART; SM00303; GPS; 1.
 DR SMART; SM00008; HormR; 1.

Db 324 CVSSPYGTLCSGPLRETRPCNNSATCPVHGVWEEWGSWSLCSRSCGRGSRSRMRTC--P 381
 Qy 274 PLNGGAFCEGQNVQKTACA-TLCPVDGWSWPWSKWSACGLDC---THWRSRECSDPAPR- 328
 | :|| ||| :| | : |||:| | | | | | | |||:| | |
 Db 382 PQHGGKACEGPELQTKLCSMAACPVEGQWLEWGPWGPCSTSCANGTQQRSRKCSVAGPAW 441
 Qy 329 -----NGGEECQ 335
 | | :
 Db 442 ATCTGALTDTRECSNLECPATDSKWGPWNAWSLCSKTCDTGWQRRFRMCQATGTQGYPC 501
 Qy 336 GTDLDTNRCTSDLC--VHSASGPEDVAL----- 361
 || : : | : | | | |
 Db 502 GTGEEVKPCSEKRCPAFHEMCRCDEYVMLMTWKKAAAGEIINYKCPPNASGSASRRCLLSA 561
 Qy 362 ----YVGLIAVAVCL---VLLLLVLILVYCRKKEGLDSDVADSSILTSGFQPVSIKPSKA 414
 | || : | | : : : : | : : : | : : | : : :
 Db 562 QGVAYWGLPSFARCISHEYRYLYLSLREHLAKQRM LAGEGMSQVVRSLQELLARTYY 620
 Qy 415 DNPHELLTIQPDLSSTTTTYYQGSCLPRQDGPSPKFQLT-----NGHLLSPLGG 461
 | : : : | | : : | | || : : : : | : || |
 Db 621 SGDLLFSVDILRNVTDTFKRATYVPSADDVQRFFQVVSFMVDAENKEKWDDAQQVSP--G 678
 Qy 462 GRHTLHHSSPTSEAEFV-----SRLSTQNYFRSLPRG-----TSNMTYGTFN 504
 | | | : | : | : | | | : | : | : | :
 Db 679 SVHLLR-----VVEDFIHLVGDALKAFQSSSLIVTDNLVISIQREPVS AVSSDITFPMRG 732
 Qy 505 FLG-----GRLMIPNTGISLLIP-----PDAIPRGK----- 530
 | | : | : || | | : | |
 Db 733 RRGMKDWVRHSEDRLF LKPEVLSLSSPGKPATSGAAGSPGRGRGPGTVPPGPGHSHQRL 792
 Qy 531 -----IYE-IYTLHKPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVIL 574
 : | : | | | | ||| : : | : | | : |
 Db 793 PADPDESSYFVIGAVLYRTLGLILPPP--RPPLAVTSRVMT--VTVRPPTQPPAEPLIT 847
 Qy 575 A-----MDHCGEPSPDSWSLRLKKQSCEGSWEDVLHLGEEAPSHLYYCQ-LEASACYV-- 626
 : : : | | : : | : | : | | | | :
 Db 848 VELSYIINGTTDPHCASWDYS-RADASSGDWD-----TENCQTLETQAAHTRC 894
 Qy 627 FTEQLGRFALVGE-----ALSVAARKRLKLLLFAPVACTSLEYNIRVYCLHDTHDALKEV 681
 : | || : : | : | : : | : | : : |
 Db 895 QCQHLSTFAVLAQPPKDLTLELAGSPSVPLVIGCAVSCMALLTLLAIYA-----AFWRF 948
 Qy 682 VQLEKQLGGQLIQEPRVLHFKDSYHNLRSLIHDVPSSLWKS KLLVSYQEIPFYHIWNGTQ 741
 : : | : : | ||| : | : : : | : : |
 Db 949 IKSERSI-----ILLNFCLSI--LASNI---LILVGQSRVLSKGVCMTMTA 988
 Qy 742 RYLHCTFTLERVSPSTSDLACKLWV-----WQVEGDG 773
 : || | | : || | :
 Db 989 AFLHFFF-----LSSFCWVLTEAWQSYLAVIGMRTRLVRKRFLCLGWGLPALV 1037
 Qy 774 QSFSINFNITKDTRFAELLALESEAG-VPALVGPSA-----FKIPFLIRQKI-----IS 821
 : | : | | : | | : | ||| : | : | : | : |
 Db 1038 VAVSVGFTRTKGYGTSSYCWLSLEGGLLYAFVGPAAVIVLVNMLIGIIVFNKLMARDGIS 1097
 Qy 822 SLDPPCRRGAD---WRTL 836
 | | : : | : |
 Db 1098 DSKKKQRAGSERC PWASL 1115

RESULT 12

TSP1_MOUSE

ID TSP1_MOUSE STANDARD; PRT; 1170 AA.
AC P35441;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thrombospondin 1 precursor.
GN THBS1 OR TSP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92128941; PubMed=1774063;
RA Lawler J., Duquette M., Ferro P., Copeland N.G., Gilbert D.J.,
RA Jenkins N.A.;
RT "Characterization of the murine thrombospondin gene.";
RL Genomics 11:587-600(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92147683; PubMed=1371115;
RA Laherty C.D., O'Rourke K., Wolf F.W., Katz R., Seldin M.F.,
RA Dixit V.M.;
RT "Characterization of mouse thrombospondin 2 sequence and expression
RT during cell growth and development.";
RL J. Biol. Chem. 267:3274-3281(1992).
RN [3]
RP SEQUENCE OF 1-490 FROM N.A.
RX MEDLINE=90375546; PubMed=2398070;
RA Bornstein P., Alfi D., Devarayalu S., Framson P., Li P.;
RT "Characterization of the mouse thrombospondin gene and evaluation of
RT the role of the first intron in human gene expression.";
RL J. Biol. Chem. 265:16691-16698(1990).
CC -!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and
CC cell-to-matrix interactions. Can bind to fibrinogen, fibronectin,
CC laminin, type V collagen and integrins alpha-V/beta-1, alpha-
CC V/beta-3 and alpha-IIb/beta-3.
CC -!- SUBUNIT: Homotrimer; disulfide-linked.
CC -!- SIMILARITY: Belongs to the thrombospondin family.
CC -!- SIMILARITY: Contains 1 VWFC domain.
CC -!- SIMILARITY: Contains 3 EGF-like domains.
CC -!- SIMILARITY: Contains 3 TSP type-1 domains.
CC -!- SIMILARITY: Contains 7 TSP type-3 domains.
CC -!- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.

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CC -----

DR EMBL; M62470; AAA50611.1; -.
 DR EMBL; M62450; AAA50611.1; JOINED.
 DR EMBL; M62451; AAA50611.1; JOINED.
 DR EMBL; M62452; AAA50611.1; JOINED.
 DR EMBL; M62453; AAA50611.1; JOINED.
 DR EMBL; M62454; AAA50611.1; JOINED.
 DR EMBL; M62455; AAA50611.1; JOINED.
 DR EMBL; M62456; AAA50611.1; JOINED.
 DR EMBL; M62457; AAA50611.1; JOINED.
 DR EMBL; M62458; AAA50611.1; JOINED.
 DR EMBL; M62459; AAA50611.1; JOINED.
 DR EMBL; M62460; AAA50611.1; JOINED.
 DR EMBL; M62461; AAA50611.1; JOINED.
 DR EMBL; M62462; AAA50611.1; JOINED.
 DR EMBL; M62463; AAA50611.1; JOINED.
 DR EMBL; M62464; AAA50611.1; JOINED.
 DR EMBL; M62465; AAA50611.1; JOINED.
 DR EMBL; M62466; AAA50611.1; JOINED.
 DR EMBL; M62467; AAA50611.1; JOINED.
 DR EMBL; M62468; AAA50611.1; JOINED.
 DR EMBL; M62469; AAA50611.1; JOINED.
 DR EMBL; M87276; AAA53063.1; -.
 DR EMBL; J05606; AAA40431.1; -.
 DR EMBL; J05605; AAA40431.1; JOINED.
 DR PIR; A40558; A40558.
 DR MGD; MGI:98737; Thbs1.
 DR GO; GO:0005615; C:extracellular space; IDA.
 DR GO; GO:0016525; P:negative regulation of angiogenesis; IDA.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR003367; tsp_3.
 DR InterPro; IPR008859; TSPC.
 DR InterPro; IPR003129; TSPN.
 DR InterPro; IPR001007; VWF_C.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00090; tsp_1; 3.
 DR Pfam; PF02412; tsp_3; 13.
 DR Pfam; PF05735; TSPC; 1.
 DR Pfam; PF02210; TSPN; 1.
 DR Pfam; PF00093; vwc; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00181; EGF; 3.
 DR SMART; SM00209; TSP1; 3.
 DR SMART; SM00210; TSPN; 1.
 DR SMART; SM00214; VWC; 1.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50026; EGF_3; 2.
 DR PROSITE; PS50092; TSP1; 3.
 DR PROSITE; PS01208; VWFC_1; 1.
 DR PROSITE; PS50184; VWFC_2; 1.
 KW Glycoprotein; Cell adhesion; Calcium-binding; Heparin-binding; Repeat;
 KW EGF-like domain; Signal.
 FT SIGNAL 1 18 POTENTIAL.

FT	CHAIN	19	1170	THROMBOSPONDIN 1.
FT	DOMAIN	19	232	HEPARIN-BINDING (POTENTIAL).
FT	DOMAIN	24	221	TSP N-TERMINAL.
FT	DOMAIN	316	373	VWFC.
FT	DOMAIN	379	429	TSP TYPE-1 1.
FT	DOMAIN	435	490	TSP TYPE-1 2.
FT	DOMAIN	492	547	TSP TYPE-1 3.
FT	DOMAIN	549	587	EGF-LIKE 1.
FT	DOMAIN	588	645	EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	646	690	EGF-LIKE 3.
FT	DOMAIN	723	758	TSP TYPE-3 1.
FT	DOMAIN	759	781	TSP TYPE-3 2.
FT	DOMAIN	782	817	TSP TYPE-3 3.
FT	DOMAIN	818	840	TSP TYPE-3 4.
FT	DOMAIN	841	878	TSP TYPE-3 5.
FT	DOMAIN	879	914	TSP TYPE-3 6.
FT	DOMAIN	915	950	TSP TYPE-3 7.
FT	DOMAIN	951	1170	C-TERMINAL.
FT	SITE	926	928	CELL ATTACHMENT SITE (POTENTIAL).
FT	DISULFID	270	270	INTERCHAIN (PROBABLE).
FT	DISULFID	274	274	INTERCHAIN (PROBABLE).
FT	DISULFID	391	423	BY SIMILARITY.
FT	DISULFID	395	428	BY SIMILARITY.
FT	DISULFID	406	413	BY SIMILARITY.
FT	DISULFID	447	484	BY SIMILARITY.
FT	DISULFID	451	489	BY SIMILARITY.
FT	DISULFID	462	474	BY SIMILARITY.
FT	DISULFID	504	541	BY SIMILARITY.
FT	DISULFID	508	546	BY SIMILARITY.
FT	DISULFID	519	531	BY SIMILARITY.
FT	DISULFID	551	562	BY SIMILARITY.
FT	DISULFID	556	572	BY SIMILARITY.
FT	DISULFID	575	586	BY SIMILARITY.
FT	DISULFID	592	608	BY SIMILARITY.
FT	DISULFID	599	617	BY SIMILARITY.
FT	DISULFID	620	644	BY SIMILARITY.
FT	DISULFID	650	663	BY SIMILARITY.
FT	DISULFID	657	676	BY SIMILARITY.
FT	DISULFID	678	689	BY SIMILARITY.
FT	DISULFID	705	713	BY SIMILARITY.
FT	DISULFID	718	738	BY SIMILARITY.
FT	DISULFID	754	774	BY SIMILARITY.
FT	DISULFID	777	797	BY SIMILARITY.
FT	DISULFID	813	833	BY SIMILARITY.
FT	DISULFID	836	856	BY SIMILARITY.
FT	DISULFID	874	894	BY SIMILARITY.
FT	DISULFID	910	930	BY SIMILARITY.
FT	DISULFID	946	1167	BY SIMILARITY.
FT	CARBOHYD	248	248	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	360	360	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	708	708	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1067	1067	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	1025	1025	F -> L (IN REF. 2).
SQ	SEQUENCE	1170	AA; 129646 MW; 0443E493615E7F06 CRC64;	

Query Match 5.6%; Score 270.5; DB 1; Length 1170;
Best Local Similarity 32.2%; Pred. No. 2.4e-12;

Matches 57; Conservative 24; Mismatches 71; Indels 25; Gaps 5;

```

Qy      207 VVRQARLADTANYTCVAKNIVAR-----RRSASAAVIVYVNGGWSTWTEWSVCSASC 258
      : :: | | : | | : : | : | : ||| | : || | : |
Db      399 IQQRGRSCDSLNNRCEGSSVQTRTCHIQECDKRFKQ-----DGGWSHWSPWSSCSVTC 451

Qy      259 GRGWQKRSRSTNPAPLNGGAFCEGQNVQKTAC-ATLCPVDGSWSPWSKWSACGLDC--- 314
      | | | | | : | | | | : | | | : | | : | | | | | : |
Db      452 GDGVITIRLCNSPSPQMNGKPCEGEARETKACKKDACPINGGWGPSPWDICSVTCGGG 511

Qy      315 THWRSRECSDPAPRNGGEECQGTDLDRNCTSDLCVHSASGPEDVALYVGLIAVAVC 371
      ||| | : : | | : | : | | | | | | | | |
Db      512 VQRRSRLCNNPTPQFGGKDCVGDVTENQVCNKQDC-----PIDGCLSNPCFAGAKC 562

```

RESULT 13

TSP1_HUMAN

ID TSP1_HUMAN STANDARD; PRT; 1170 AA.
AC P07996; Q15667;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Thrombospondin 1 precursor.
GN THBS1 OR TSP1 OR TSP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endothelial cells;
RX MEDLINE=87057617; PubMed=2430973;
RA Lawler J., Hynes R.O.;
RT "The structure of human thrombospondin, an adhesive glycoprotein with
RT multiple calcium-binding sites and homologies with several different
RT proteins.";
RL J. Cell Biol. 103:1635-1648(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89139590; PubMed=2918029;
RA Hennessy S.W., Frazier B.A., Kim D.D., Deckwerth T.L.,
RA Baumgartel D.M., Rotwein P., Frazier W.A.;
RT "Complete thrombospondin mRNA sequence includes potential regulatory
RT sites in the 3' untranslated region.";
RL J. Cell Biol. 108:729-736(1989).
RN [3]
RP SEQUENCE OF 1-397 FROM N.A.
RX MEDLINE=87157592; PubMed=3030396;
RA Kobayashi S., Eden-Mccutchan F., Framson P., Bornstein P.;
RT "Partial amino acid sequence of human thrombospondin as determined by
RT analysis of cDNA clones: homology to malarial circumsporozoite
RT proteins.";
RL Biochemistry 25:8418-8425(1986).
RN [4]
RP SEQUENCE OF 1-374 FROM N.A.
RX MEDLINE=86287276; PubMed=3461443;
RA Dixit V.M., Hennessy S.W., Grant G.A., Rotwein P., Frazier W.A.;

RT "Characterization of a cDNA encoding the heparin and collagen binding
 RT domains of human thrombospondin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:5449-5453(1986).
 RN [5]
 RP SEQUENCE OF 1-166 FROM N.A.
 RX MEDLINE=89291870; PubMed=2544587;
 RA Laherty C.D., Gierman T.M., Dixit V.M.;
 RT "Characterization of the promoter region of the human thrombospondin
 RT gene. DNA sequences within the first intron increase transcription.";
 RL J. Biol. Chem. 264:11222-11227(1989).
 RN [6]
 RP SEQUENCE OF 1028-1170 FROM N.A.
 RA la Fleur M., Jobin C., Gauthier J., Kreis C.G.;
 RL Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
 RN [7]
 RP CARBOHYDRATE-LINKAGE SITES TRP-385; SER-394; TRP-438; TRP-441;
 RP THR-450; TRP-498 AND THR-507.
 RC TISSUE=Platelet;
 RX MEDLINE=21125860; PubMed=11067851;
 RA Hofsteenge J., Huwiler K.G., Macek B., Hess D., Lawler J.,
 RA Mosher D.F., Peter-Katalinic J.;
 RT "C-mannosylation and O-fucosylation of the thrombospondin type 1
 RT module.";
 RL J. Biol. Chem. 276:6485-6498(2001).
 RN [8]
 RP THROMBOSPONDIN DOMAIN DISULFIDE BRIDGES.
 RX MEDLINE=22338361; PubMed=12450399;
 RA Huwiler K.G., Vestling M.M., Annis D.S., Mosher D.F.;
 RT "Biophysical characterization, including disulfide bond assignments,
 RT of the anti-angiogenic type 1 domains of human thrombospondin-1.";
 RL Biochemistry 41:14329-14339(2002).
 CC -!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and
 CC cell-to-matrix interactions. Can bind to fibrinogen, fibronectin,
 CC laminin, type V collagen and integrins alpha-V/beta-1, alpha-
 CC V/beta-3 and alpha-IIb/beta-3.
 CC -!- SUBUNIT: Homotrimer; disulfide-linked.
 CC -!- SIMILARITY: Belongs to the thrombospondin family.
 CC -!- SIMILARITY: Contains 1 VWFC domain.
 CC -!- SIMILARITY: Contains 3 EGF-like domains.
 CC -!- SIMILARITY: Contains 3 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 7 TSP type-3 domains.
 CC -!- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
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 CC -----
 DR EMBL; M25631; AAA36741.1; -.
 DR EMBL; X04665; CAA28370.1; -.
 DR EMBL; X14787; CAA32889.1; -.
 DR EMBL; M14326; AAA61237.1; ALT_SEQ.
 DR EMBL; J04835; AAA61178.1; -.
 DR EMBL; M99425; AAB59366.1; -.

DR PIR; A26155; TSHUP1.
 DR PDB; 1LSL; 18-DEC-02.
 DR GlycoSuiteDB; P07996; -.
 DR Genew; HGNC:11785; THBS1.
 DR MIM; 188060; -.
 DR GO; GO:0004866; F:endopeptidase inhibitor activity; TAS.
 DR GO; GO:0004871; F:signal transducer activity; TAS.
 DR GO; GO:0007275; P:development; TAS.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR003367; tsp_3.
 DR InterPro; IPR008859; TSPC.
 DR InterPro; IPR003129; TSPN.
 DR InterPro; IPR001007; VWF_C.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00090; tsp_1; 3.
 DR Pfam; PF02412; tsp_3; 13.
 DR Pfam; PF05735; TSPC; 1.
 DR Pfam; PF02210; TSPN; 1.
 DR Pfam; PF00093; vwc; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00181; EGF; 3.
 DR SMART; SM00209; TSP1; 3.
 DR SMART; SM00210; TSPN; 1.
 DR SMART; SM00214; VWC; 1.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50026; EGF_3; 2.
 DR PROSITE; PS50092; TSP1; 3.
 DR PROSITE; PS01208; VWFC_1; 1.
 DR PROSITE; PS50184; VWFC_2; 1.
 KW Glycoprotein; Cell adhesion; Calcium-binding; Heparin-binding; Repeat;
 KW EGF-like domain; Signal; 3D-structure.
 FT SIGNAL 1 18
 FT CHAIN 19 1170 THROMBOSPONDIN 1.
 FT DOMAIN 19 232 HEPARIN-BINDING (POTENTIAL).
 FT DOMAIN 24 221 TSP N-TERMINAL.
 FT DOMAIN 316 373 VWFC.
 FT DOMAIN 379 429 TSP TYPE-1 1.
 FT DOMAIN 435 490 TSP TYPE-1 2.
 FT DOMAIN 492 547 TSP TYPE-1 3.
 FT DOMAIN 549 587 EGF-LIKE 1.
 FT DOMAIN 588 645 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 646 690 EGF-LIKE 3.
 FT DOMAIN 723 758 TSP TYPE-3 1.
 FT DOMAIN 759 781 TSP TYPE-3 2.
 FT DOMAIN 782 817 TSP TYPE-3 3.
 FT DOMAIN 818 840 TSP TYPE-3 4.
 FT DOMAIN 841 878 TSP TYPE-3 5.
 FT DOMAIN 879 914 TSP TYPE-3 6.
 FT DOMAIN 915 950 TSP TYPE-3 7.
 FT DOMAIN 951 1170 C-TERMINAL.
 FT SITE 926 928 CELL ATTACHMENT SITE (POTENTIAL).
 FT DISULFID 270 270 INTERCHAIN (PROBABLE).

FT	DISULFID	274	274	INTERCHAIN (PROBABLE).
FT	DISULFID	391	423	
FT	DISULFID	395	428	
FT	DISULFID	406	413	
FT	DISULFID	447	484	
FT	DISULFID	451	489	
FT	DISULFID	462	474	
FT	DISULFID	504	541	
FT	DISULFID	508	546	
FT	DISULFID	519	531	
FT	DISULFID	551	562	BY SIMILARITY.
FT	DISULFID	556	572	BY SIMILARITY.
FT	DISULFID	575	586	BY SIMILARITY.
FT	DISULFID	592	608	BY SIMILARITY.
FT	DISULFID	599	617	BY SIMILARITY.
FT	DISULFID	620	644	BY SIMILARITY.
FT	DISULFID	650	663	BY SIMILARITY.
FT	DISULFID	657	676	BY SIMILARITY.
FT	DISULFID	678	689	BY SIMILARITY.
FT	DISULFID	705	713	BY SIMILARITY.
FT	DISULFID	718	738	BY SIMILARITY.
FT	DISULFID	754	774	BY SIMILARITY.
FT	DISULFID	777	797	BY SIMILARITY.
FT	DISULFID	813	833	BY SIMILARITY.
FT	DISULFID	836	856	BY SIMILARITY.
FT	DISULFID	874	894	BY SIMILARITY.
FT	DISULFID	910	930	BY SIMILARITY.
FT	DISULFID	946	1167	BY SIMILARITY.
FT	CARBOHYD	248	248	N-LINKED (GLCNAC. . .).
FT	CARBOHYD	360	360	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	385	385	C-LINKED (MAN).
FT				/FTid=CAR_000205.
FT	CARBOHYD	394	394	O-LINKED (FUC. . .).
FT				/FTid=CAR_000206.
FT	CARBOHYD	438	438	C-LINKED (MAN).
FT				/FTid=CAR_000207.
FT	CARBOHYD	441	441	C-LINKED (MAN).
FT				/FTid=CAR_000208.
FT	CARBOHYD	450	450	O-LINKED (FUC. . .).
FT				/FTid=CAR_000209.
FT	CARBOHYD	498	498	C-LINKED (MAN).
FT				/FTid=CAR_000210.
FT	CARBOHYD	507	507	O-LINKED (FUC. . .).
FT				/FTid=CAR_000211.
FT	CARBOHYD	708	708	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1067	1067	N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 5.6%; Score 268.5; DB 1; Length 1170;
 Best Local Similarity 32.9%; Pred. No. 3.4e-12;
 Matches 51; Conservative 24; Mismatches 61; Indels 19; Gaps 4;

Qy	207	VVRQARLADTANYTCVAKNIVAR-----RRSASAAVIVYVNGGWSTWTEWSVCSASC	258
		: :: : :: : : : :	
Db	399	IQQRGRSCDSLNNRCEGSSVQTRTCHIQCCKRFKQ-----DGGWSHWSPWSSCSVTC	451
Qy	259	GRGWQKRSRSTNPAPLNGGAFCEGQNVQKTAC-ATLCPVDGSWSPWSKWSACGLDC---	314
		: : : : :	

Db 452 GDGVITRIRLCNSPSPQMNGKPCEGEARETKACKKDACPINGGWGPWSPWDICSVTCGGG 511

Qy 315 THWRSRECSDPAPRNGGEECQGTDLDTNRNCTSDLC 349

Db 512 VQKRSRLCNNPTPQFGGKDCVGDVTENQICNKQDC 546

RESULT 14

TSP1_BOVIN

ID TSP1_BOVIN STANDARD; PRT; 1170 AA.

AC Q28178; Q28179;

DT 01-NOV-1997 (Rel. 35, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Thrombospondin 1 precursor.

GN THBS1 OR TSP1 OR TSP-1.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Holstein; TISSUE=Tooth;

RX MEDLINE=98173773; PubMed=9507054;

RA Ueno A., Yamashita K., Nagata T., Tsurumi C., Miwa Y., Kitamura S.,

RA Inoue H.;

RT "cDNA cloning of bovine thrombospondin 1 and its expression in

RT odontoblasts and predentin.";

RL Biochim. Biophys. Acta 1382:17-22(1998).

RN [2]

RP SEQUENCE OF 1-18 AND 710-1170 FROM N.A.

RC TISSUE=Aortic endothelium;

RA Zafar R.S., Moll Y.D., Womack J.F., Walz D.A.;

RL Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and

CC cell-to-matrix interactions. Can bind to fibrinogen, fibronectin,

CC laminin, type V collagen and integrins alpha-V/beta-1, alpha-

CC V/beta-3 and alpha-IIb/beta-3. May play a role in dentinogenesis

CC and/or maintenance of dentin and dental pulp.

CC -!- SUBUNIT: Homotrimer; disulfide-linked.

CC -!- TISSUE SPECIFICITY: Odontoblasts.

CC -!- SIMILARITY: Belongs to the thrombospondin family.

CC -!- SIMILARITY: Contains 1 VWFC domain.

CC -!- SIMILARITY: Contains 3 EGF-like domains.

CC -!- SIMILARITY: Contains 3 TSP type-1 domains.

CC -!- SIMILARITY: Contains 7 TSP type-3 domains.

CC -!- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; AB005287; BAA21115.1; -.
 DR EMBL; X87618; CAA60950.1; -.
 DR EMBL; X87619; CAA60951.1; -.
 DR PIR; S55501; S55501.
 DR GlycoSuiteDB; Q28178; -.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR003367; tsp_3.
 DR InterPro; IPR008859; TSPC.
 DR InterPro; IPR003129; TSPN.
 DR InterPro; IPR001007; VWF_C.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00090; tsp_1; 3.
 DR Pfam; PF02412; tsp_3; 13.
 DR Pfam; PF05735; TSPC; 1.
 DR Pfam; PF02210; TSPN; 1.
 DR Pfam; PF00093; vwc; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00181; EGF; 3.
 DR SMART; SM00209; TSP1; 3.
 DR SMART; SM00210; TSPN; 1.
 DR SMART; SM00214; VWC; 1.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50026; EGF_3; 2.
 DR PROSITE; PS50092; TSP1; 3.
 DR PROSITE; PS01208; VWFC_1; 1.
 DR PROSITE; PS50184; VWFC_2; 1.
 KW Glycoprotein; Cell adhesion; Calcium-binding; Heparin-binding; Repeat;
 KW EGF-like domain; Signal.

FT	SIGNAL	1	18	BY SIMILARITY.
FT	CHAIN	19	1170	THROMBOSPONDIN 1.
FT	DOMAIN	19	232	HEPARIN-BINDING (POTENTIAL).
FT	DOMAIN	24	221	TSP N-TERMINAL.
FT	DOMAIN	316	373	VWFC.
FT	DOMAIN	379	429	TSP TYPE-1 1.
FT	DOMAIN	435	490	TSP TYPE-1 2.
FT	DOMAIN	492	547	TSP TYPE-1 3.
FT	DOMAIN	549	587	EGF-LIKE 1.
FT	DOMAIN	588	645	EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	646	690	EGF-LIKE 3.
FT	DOMAIN	723	758	TSP TYPE-3 1.
FT	DOMAIN	759	781	TSP TYPE-3 2.
FT	DOMAIN	782	817	TSP TYPE-3 3.
FT	DOMAIN	818	840	TSP TYPE-3 4.
FT	DOMAIN	841	878	TSP TYPE-3 5.
FT	DOMAIN	879	914	TSP TYPE-3 6.
FT	DOMAIN	915	950	TSP TYPE-3 7.
FT	DOMAIN	951	1170	C-TERMINAL.
FT	SITE	926	928	CELL ATTACHMENT SITE (POTENTIAL).
FT	DISULFID	270	270	INTERCHAIN (PROBABLE).
FT	DISULFID	274	274	INTERCHAIN (PROBABLE).
FT	DISULFID	391	423	BY SIMILARITY.
FT	DISULFID	395	428	BY SIMILARITY.

FT	DISULFID	406	413	BY SIMILARITY.
FT	DISULFID	447	484	BY SIMILARITY.
FT	DISULFID	451	489	BY SIMILARITY.
FT	DISULFID	462	474	BY SIMILARITY.
FT	DISULFID	504	541	BY SIMILARITY.
FT	DISULFID	508	546	BY SIMILARITY.
FT	DISULFID	519	531	BY SIMILARITY.
FT	DISULFID	551	562	BY SIMILARITY.
FT	DISULFID	556	572	BY SIMILARITY.
FT	DISULFID	575	586	BY SIMILARITY.
FT	DISULFID	592	608	BY SIMILARITY.
FT	DISULFID	599	617	BY SIMILARITY.
FT	DISULFID	620	644	BY SIMILARITY.
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FT	DISULFID	705	713	BY SIMILARITY.
FT	DISULFID	718	738	BY SIMILARITY.
FT	DISULFID	754	774	BY SIMILARITY.
FT	DISULFID	777	797	BY SIMILARITY.
FT	DISULFID	813	833	BY SIMILARITY.
FT	DISULFID	836	856	BY SIMILARITY.
FT	DISULFID	874	894	BY SIMILARITY.
FT	DISULFID	910	930	BY SIMILARITY.
FT	DISULFID	946	1167	BY SIMILARITY.
FT	CARBOHYD	248	248	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	360	360	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	708	708	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1067	1067	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1085	1085	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	805	805	S -> G (IN REF. 2).
SQ	SEQUENCE	1170 AA;	129533 MW;	0DD6ADF3E5FA031A CRC64;

Query Match 5.5%; Score 265.5; DB 1; Length 1170;

Best Local Similarity 32.9%; Pred. No. 5.8e-12;

Matches 51; Conservative 24; Mismatches 61; Indels 19; Gaps 4;

Qy	207	VVRQARLADTANYTCVAKNIVAR-----RRSASAAVIVYVNGGWSTWTEWSVCSASC	258
		: :: : : : : : : :	
Db	399	IQQRGRSCDSLNNRCEGSSVQTRTCHIQCCKRFKQ-----DGGWSHWSPWSSCSVTC	451
Qy	259	GRGWQKRSRSCCTNPAPLNGGAFCEGQNVQKTAC-ATLCPVDGSWSPWSKWSACGLDC---	314
		: : : : : : :	
Db	452	GDGVITRIRLCNSPSPQMNGKPCGKARETKACQKDCSPINGGWGPWSPWDICSVTCGGG	511
Qy	315	THWRSRECSDPAPRNGGEECQGTDLDTNRCTSDLC	349
		: : : : :	
Db	512	VQKRSRLCNNPKPQFGGKDCVGDVTENQICNKQDC	546

RESULT 15

TSP2_CHICK

ID TSP2_CHICK STANDARD; PRT; 1178 AA.

AC P35440;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Thrombospondin 2 precursor.
 GN THBS2 OR TSP2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91217026; PubMed=2022631;
 RA Lawler J., Duquette M., Ferro P.;
 RT "Cloning and sequencing of chicken thrombospondin."
 RL J. Biol. Chem. 266:8039-8043(1991).
 CC -!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and
 CC cell-to-matrix interactions. Can bind to fibrinogen, fibronectin,
 CC laminin and type V collagen.
 CC -!- SUBUNIT: Homotrimer; disulfide-linked.
 CC -!- SIMILARITY: Belongs to the thrombospondin family.
 CC -!- SIMILARITY: Contains 1 VWFC domain.
 CC -!- SIMILARITY: Contains 3 EGF-like domains.
 CC -!- SIMILARITY: Contains 3 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 7 TSP type-3 domains.
 CC -!- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
 CC -----
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 CC -----
 DR EMBL; M60853; AAA51437.1; -.
 DR PIR; A39804; A39804.
 DR HSSP; P00740; 1EDM.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR003367; tsp_3.
 DR InterPro; IPR008859; TSPC.
 DR InterPro; IPR003129; TSPN.
 DR InterPro; IPR001007; VWF_C.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00090; tsp_1; 3.
 DR Pfam; PF02412; tsp_3; 13.
 DR Pfam; PF05735; TSPC; 1.
 DR Pfam; PF02210; TSPN; 1.
 DR Pfam; PF00093; vwc; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00209; TSP1; 3.
 DR SMART; SM00210; TSPN; 1.
 DR SMART; SM00214; VWC; 1.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 1.

DR	PROSITE; PS50026; EGF_3; 2.		
DR	PROSITE; PS50092; TSP1; 3.		
DR	PROSITE; PS01208; VWFC_1; 1.		
DR	PROSITE; PS50184; VWFC_2; 1.		
KW	Glycoprotein; Cell adhesion; Calcium-binding; Heparin-binding; Repeat;		
KW	EGF-like domain; Signal.		
FT	SIGNAL	1 22	POTENTIAL.
FT	CHAIN	23 1178	THROMBOSPONDIN 2.
FT	DOMAIN	25 221	TSP N-TERMINAL.
FT	DOMAIN	? 232	HEPARIN-BINDING (POTENTIAL).
FT	DOMAIN	324 381	VWFC.
FT	DOMAIN	387 437	TSP TYPE-1 1.
FT	DOMAIN	443 498	TSP TYPE-1 2.
FT	DOMAIN	500 555	TSP TYPE-1 3.
FT	DOMAIN	555 595	EGF-LIKE 1.
FT	DOMAIN	596 653	EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	654 698	EGF-LIKE 3.
FT	DOMAIN	731 766	TSP TYPE-3 1.
FT	DOMAIN	767 789	TSP TYPE-3 2.
FT	DOMAIN	790 825	TSP TYPE-3 3.
FT	DOMAIN	826 848	TSP TYPE-3 4.
FT	DOMAIN	849 886	TSP TYPE-3 5.
FT	DOMAIN	887 922	TSP TYPE-3 6.
FT	DOMAIN	923 958	TSP TYPE-3 7.
FT	DOMAIN	959 1178	C-TERMINAL.
FT	SITE	934 935	CELL ATTACHMENT SITE (POTENTIAL).
FT	DISULFID	399 431	BY SIMILARITY.
FT	DISULFID	403 436	BY SIMILARITY.
FT	DISULFID	414 421	BY SIMILARITY.
FT	DISULFID	455 492	BY SIMILARITY.
FT	DISULFID	459 497	BY SIMILARITY.
FT	DISULFID	470 482	BY SIMILARITY.
FT	DISULFID	512 549	BY SIMILARITY.
FT	DISULFID	516 554	BY SIMILARITY.
FT	DISULFID	527 539	BY SIMILARITY.
FT	DISULFID	559 570	BY SIMILARITY.
FT	DISULFID	564 580	BY SIMILARITY.
FT	DISULFID	583 594	BY SIMILARITY.
FT	DISULFID	600 616	BY SIMILARITY.
FT	DISULFID	607 625	BY SIMILARITY.
FT	DISULFID	628 652	BY SIMILARITY.
FT	DISULFID	658 671	BY SIMILARITY.
FT	DISULFID	665 684	BY SIMILARITY.
FT	DISULFID	686 697	BY SIMILARITY.
FT	DISULFID	713 721	BY SIMILARITY.
FT	DISULFID	726 746	BY SIMILARITY.
FT	DISULFID	762 782	BY SIMILARITY.
FT	DISULFID	785 805	BY SIMILARITY.
FT	DISULFID	821 841	BY SIMILARITY.
FT	DISULFID	844 864	BY SIMILARITY.
FT	DISULFID	882 902	BY SIMILARITY.
FT	DISULFID	918 938	BY SIMILARITY.
FT	DISULFID	954 1175	BY SIMILARITY.
FT	CARBOHYD	157 157	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	244 244	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	317 317	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	322 322	N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 590 590 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 716 716 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1075 1075 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1178 AA; 131816 MW; F37E02F42C8717A2 CRC64;

Query Match 5.5%; Score 263; DB 1; Length 1178;
 Best Local Similarity 36.2%; Pred. No. 9.1e-12;
 Matches 58; Conservative 16; Mismatches 70; Indels 16; Gaps 5;

Qy 210 QARLADTANYTCVAKNIVARRRS-ASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRS 268
 : | | | : | | | : : ||| | : || || : || | | |
 Db 410 RGRSCDVTRSACTGPHIQTRMCSEKCDHRIRQDGGWSHWSPWSSCSVTCGVGNITRIRL 469

 Qy 269 CTNPAPLNGGAFCEGQNVQKTACATL-CPVDGSWSPWSKWSACGLDC---THWRSRECS 324
 | : | | | | : | | | : | | | | | : | | | | :
 Db 470 CNSPIPQMGGKNCVGNGRETEKCEKAPCPVNGQWGPWSPWSACTVTCGGGIRERSRLCNS 529

 Qy 325 PAPRNGGEECQGTDLDT-----RNCTSDLCVHSASGP 356
 | | : || : | | | | : | | | : : |
 Db 530 PEPQYGGKPCVG---DTKQHDMCNKRDCPIDGCLSNPCFP 566

Search completed: July 6, 2004, 14:33:55
 Job time : 19 secs